Bee Communities in Restored Landfill Sites of Niagara Region

by

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ABSTRACT

This study examined the impact of habitat restoration on bee communities (Hymenoptera: Apidae) of the Niagara Region, Ontario, Canada. Bee abundance and diversity was studied in three restored landfill sites: the Glenridge Quarry Naturalization Site (GQNS) in St. Catharines, Elm Street Naturalization Site in Port Colborne, and Station Road Naturalization Site in Wainfleet during 2011 and 2012. GQNS represented older sites restored from 2001-2003. Elm and Station sites represented newly restored landfills as of 2011. These sites were compared to control sites at Brock University where bee communities are well established and again to other landfills where no stable habitat was available before restoration. The objective of this study is to investigate the impact of restoration level on bee abundance and diversity in restored landfill sites of the Niagara Region. Based on the increased disturbance hypothesis (InDH) and the intermediate disturbance hypothesis (IDH), I hypothesized that bee abundance and diversity will follow two patterns. First pattern according to InDH suggest that as the disturbance decrease the bee abundance and diversity will increased. Second pattern according to the IDH bee abundance and diversity will be the highest at the intermediate level of disturbance. A total of 7 173 bees were collected using pan traps and flower collections, from May to October 2011 and 2012. Bees were classified to five families, 21 genera and sub-genera, containing at least 78 species. In 2011 bee abundance was not significantly different among restoration levels while in 2012 bee abundance was significant difference among restoration level. According to family there were no significant differences in Halictidae and Apidae abundance among restoration level while Colletidae and Megachilidae abundance were varied among restoration levels. The bee species richness

was highest in the newly restored sites followed by restored control sites, and then the control site. The current study demonstrates that habitat restoration results in rapid increases in bee abundance and diversity for newly restored sites, and, further, that it takes only 2-3 years for bee assemblages in newly restored sites to arrive at the same levels of abundance and diversity as in nearby control sites where bee communities are well established.

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1.1. Disturbance

Disturbance can be identified as changes in the environmental conditions of an ecosystem which affect the quantity and quality of resources, which ultimately impact the biodiversity of the habitat (Svensson et al., 2012; White et al., 1997). Perturbations can create a variety of environmental conditions by refreshing limited resources and removing dominant species (Levin & Paine, 1974), resulting in increased species diversity and abundance. Disturbances expose new areas for colonization by releasing natural resources in different patches and at different times, which causes heterogeneity (Sousa, 1984). Disturbances cause fluctuations in ecological patterns and processes.

1.2. Human impact on ecosystems

The disturbances caused by humans continue to cause global ecological concerns because of how these affect and change the dynamics and structure of ecosystems. Perturbations can result in loss of habitat, reduction of habitat quality, and fragmentation (Kearns et al., 1998; White et al., 1997). The perturbations caused by modern agricultural practices, pesticides (Kearns et al., 1998), invasions of non-native plants and animals (Manchester & Bullock, 2000), urbanization (McKinney, 2002), recreation, livestock (Cooper et al., 2005), prescribed fire, pollution (Mouratov, et al., 2008), mining, industry, harvest, logging, roads (Vos & Chardon, 1998), and many other modifications caused by humans are associated with negative consequences for biodiversity (Mora & Sale, 2011).

1.3. The importance of arthropods

Arthropods are an ideal model to study human impacts on ecosystems. Arthropods are abundant, good responders to environmental change, and they have a

short generation time (McIntyre et al., 2001). Arthropods have important roles in an ecosystem's functioning such as pollination, food web vectors, movement and exchange of organic and inorganic matter (McIntyre et al., 2001).

Insects are the most important pollinators in most habitats. It is estimated that 80% of all human food sources depend, directly or indirectly, on insect pollination (Thomson, 2001). The economies of many communities, and even whole countries, are sometimes dependent on how well local pollinators are able to pollinate crops which provide food for humans and livestock (Kevan, 1999; Williams et al., 2001). For example, the value of native insects of the United States has been estimated at $57 billion (Losey & Vaughan, 2006). Insect pollination is essential in the maintenance of biodiversity because of its importance in plant reproduction, which can require specific pollinators. Some insects are keystone species that play a critical role in their ecosystems, which makes conservation a necessary mission (You et al., 2005).

1.4. The special value of bees

There are more than 25,000 bee species that belong to seven bee families in the world (Danforth et al., 2006; Michener, 2000; Williams et al., 2001). Six families are found in North America (Grundel et al., 2010). The importance of bees as pollinators is well known in many ecosystems (Kremen et al., 2002). Bee communities are sensitive to anthropogenic disturbance, and they respond quickly to environmental changes (Quintero et al., 2010). Bee assemblages are valuable bioindicators of the environment's health and their diversity is representative of the diversity within an ecosystem as a whole (Duelli & Obrist, 1998; Kevan 1999; Richards et al., 2011).

Recently, the issue of the decline of pollinators has received considerable attention within the scientific community and news media. Pollinator decline has been defined as a decrease in the size of the pollinator populations for a particular habitat. Bees are in decline partly due to habitat loss (Winfree et al., 2009), a result of losses of nesting sites and the deprivation of vegetation that bees rely on for nectar and pollen resources (Steffan-Dewenter & Tscharntke, 2001). Global agricultural production may suffer if the continual decline in pollinator numbers continues (Aizen & Haeder, 2009). Specialist species of pollinator suffer the most when there is ecosystem damage, but the ecosystem suffers more when the generalist species are damaged because several different types of flowers will be affected (Dxion, 2009). Insect pollination, therefore, has implications for the economy, food security, and biodiversity.

1.5. The influence of disturbance on abundance and diversity

Many studies suggest bee species abundance, richness, and composition change after severe disturbances. Bee diversity and abundance are subject to change through succession as a result of variation in vegetation type. Species richness is used as a measurement to quantify biodiversity (Svensson et al., 2012) and to track changes in community structure and composition (You et al., 2009).

1.5.1. Influence of disturbance on abundance

Generally, there is a decrease in abundance as a result of disturbance, but once the perturbation stops, abundance starts to increase rapidly (Hopwood, 2008). Disturbed habitats in Patagonia, Argentina have a higher numbers of bees and bee species than undisturbed habitats (Quintero et al., 2010).

Hill and his colleagues (1995) observed a decline in abundance of butterflies in lowland monsoon forest in Buru, Indonesia due to clear cutting. Disturbances may actually create new habitats or habitat heterogeneity favourable for more bee species at an intermediate time after recovery, but while the disturbance levels are still high, species are at risk of becoming extinct (Wimberly, 2006).

1.5.2. Influence of disturbance on diversity

Changes in the diversity of bee communities during succession after disturbance may be predicted by two models. The first, the Increasing Disturbance Hypothesis (InDH) states that increased disturbance will decrease species richness (Gray, 1989). Death and Winterbourn (1995) found that invertebrate diversity decreased with increased disturbance in a study in New Zealand. When the effects of grazing intensity in grasslands of north Germany were studied, insect abundance and diversity were found to be higher in the areas of lowest grazing intensity (Kruess & Tscharntke, 2002). Areas ungrazed over the long term had the highest diversity, supporting the hypothesis that disturbance decreases abundance and diversity. Another study done by Simmons (1999) linked arthropod diversity to succession. They found that arthropod diversity was linked to plant diversity, which increased significantly with field succession age (Simmons, 1999). A study performed by Schwilk et al. (1997) sought to validate the InDH by studying diversity in African grasslands called fynbos, which are routinely disturbed by fire. Frequently burned sites were compared to sites burned less frequently. The InDH described the species richness patterns: the highest species richness was recovered in the least disturbed sites (Schwilk et al. 1997). Also, Ikeda (2003) studied the species richness of herbaceous plant communities in Tokyo, Japan. He found that the disturbance reduced

the abundance and diversity of herbaceous plants. Kerr and Packer (2000) found that butterfly diversity was strongly linked to bee diversity. Steffan-Dewenter and Tscharntke (1997) studied the early succession of butterfly and plant communities on set-aside fields in south Germany. They found that butterfly colonization mainly depended on the availability of food plants which changed with the age of the field. Also, they found that species diversity of butterflies was higher in the late succession fields than the early succession and pioneer fields. The highest diversity of butterflies in the late succession fields occurred due to the highest abundance and diversity of flowering plants in these fields (Steffan-Dewenter & Tscharntke, 1997). After anthropogenic disturbances, species diversity increases as a result of restoration since native species abundance increases and non-native species decrease (Gibson et al., 2000).

The second model, the Intermediate Disturbance Hypothesis (IDH), states that areas experiencing intermediate levels of disturbance have the greatest biodiversity followed by areas with low disturbance levels, while areas with the highest disturbance levels have the least biodiversity (Connell, 1978). The intermediate disturbance hypothesis (IDH) was introduced by Connell (1978) to explain the effect of disturbance on tropical rain forest and coral reef diversity, both of which ranked as high species richness ecosystems. There were three different measurements of disturbances: frequency of disturbance, time between disturbances, and intensity of disturbance (Connell, 1978). At a high disturbance level, only a few species with a special colonization abilities such as adaptation to the rapid environmental changes survived (Connell, 1978). At intermediate levels of disturbance, a variety of species can survive (Connell, 1978). When more time is allowed to pass and the site is considered low disturbance (i.e., more than

three years as Rutgers-Kelly & Richards (2013) suggest), the species richness decreases because pioneer species are removed by late succession competitive species (Connell, 1978). High diversity can be achieved only when species with good dispersal, but poor competitive abilities coexist with highly competitive species (Connell, 1978). Succession can lead to an increase in the availability of new niches that could be favourable to different species, thereby allowing more species preservation (Connell 1978). The intermediate level of disturbance had the highest species richness, as well as species from both low and high disturbance levels (Connell, 1978). Svensson et al. (2007) argued that the highest species richness could be found at an intermediate frequency of disturbance. The moderate level of disturbance is generally important for habitat heterogeneity to ensure the highest levels of biodiversity (Benton et al., 2003).

1.5.3. Influence of disturbance on community composition

Bee community composition is defined as the proportion of bee species relative to total species in a given area (Williams et al., 2001). The degree of disturbance caused by land use can change the bee community composition (Brosi et al., 2008). Disturbances affect the community structure located at the disturbed patch by changing the succession stage and abundance (Sousa, 1979). A study done by Cardinale et al. (2000) suggests that perturbations cause changing environmental conditions which affect community composition. In the coastal stream of southern California, physical disturbance affected community composition (i.e. relative abundance of filter feeding insects with *Simulium virgatum* and *Hydrosyche oslari* dominating the coastal stream) (Hemphill & Cooper, 1983). Usually, when there is new space available, it is colonized quickly by *Simulium virgatum*. When the time from the last disturbance is increased, the number of *Simulium*

virgatum decreases, while the abundance of *Hydrosyche oslari* increases (Hemphill & Cooper, 1983).

A study by Larsen et al. (2005) tested how loss of habitat affects the community structure of beetles in tropical forests and bees in temperate agro-natural landscapes. The beetles were studied in Lago Guri, located in Bolivar, Venezuela, while the wild bees were studied from organic and conventional watermelon farm sites in Yolo County, California, USA. The beetles were studied in 29 islands that varied in size. The islands were disturbed by construction of hydroelectric dams which were flooded in 1986. The bees were collected from natural habitats and agricultural areas. Bee abundance and diversity declined as the natural habitat declined. In addition, they found a positive correlation between abundance and species richness in both beetles and bees. Local extinctions of dung beetles and bees occurred as a result of disturbance. The extinction rate of the larger sized species was higher than for smaller sized species. In conclusion, they found that abundance and species richness of beetle and bee communities changed in response to anthropogenic disturbance (Larsen et al., 2005).

Disturbance by fire has a positive effect on arthropod diversity. Ferrenberg et al. (2006) investigated the effects of disturbance caused by prescribed fire on arthropod abundance and diversity. Fire can affect arthropods directly by killing them and indirectly by changing resources and resulting in a new habitat (Ferrenberg et al., 2006). Overall, arthropod abundance was lower in burned treatments than the unburned controls (Ferrenberg et al., 2006). Species richness was greater in burn treatments than in controls, and these areas had fewer dominant species (Ferrenberg et al., 2006).

Another study by Moretti et al. (2004) found evidence to support IDH. This study confirmed that the diversity of bees and wasps in southern Switzerland was highest in sites burned at medium frequencies where rare species were present, unlike either unburned sites or sites burned at high frequency which had lower diversity. Sites with intermediate levels of disturbance resulting from fire supported higher species richness than unburned sites (Moretti et al., 2004).

Potts et al. (2003a) studied the effects of fire on plant-pollinator communities in the Mount Carmel National Reserve, Israel. Two years after a burn, they found vegetation and species richness increasing, followed by an immediate decrease in richness. The intermediate disturbance hypothesis was confirmed that numbers of species and individuals tend to be higher in the first few years after fire compared to unburned sites (Potts et al., 2003a). Muona and Rutanen (1994) studied three burned areas located within Siberian taiga forest in Finland. Fire disturbance caused an increase in abundance and diversity of boreal coniferous forest beetles (Muona & Rutanen, 1994). They found that abundance and diversity of many species rapidly increased after fire (e.g. predators living in litter and mushrooms, and wood-boring, soil dwelling, and fire specialist species) (Muona & Rutanen, 1994). Another study done by Koponen (2005) on the spider community at Tammela, Riihivalkama, east of the Torronsuo National Park in Finland, found that the spider communities at the burned sites were higher in abundance and diversity than in control sites. Also, the spider community in the burned sites was very different than the control sites in the three years following fire (Koponen, 2005). Buddle et al. (2000) found that spider communities were higher in abundance following tree harvest than in control sites in the mid-boreal mixed-wood forests of Alberta.

Carvell (2002) studied the effect of disturbance created by cattle grazing and vehicle activity on habitat characteristics which influenced the abundance, diversity, and foraging activity of bumblebees. The study was carried out in the Salisbury Plain training area of England. A total of 475 species of bumblebees were observed. The most abundant were *B. lucorum*, *B. lapidarius*, and *B. terrestris.* All were *Bombus* species of the mainland found in the disturbed sites, but their relative abundance was different. The differences in bee communities between the mainland and the disturbed sites were due to the bumble bee habitat availability. The disturbed sites had more plentiful vegetation and more flowering plant species than the mainland, two factors highly linked to bumblebee abundance and diversity. Carvell (2002) helped to explain the important role of small-scale disturbances in increasing bumblebee abundance and diversity.

Liow et al. (2001) studied bee diversity in disturbed sites. They surveyed bee communities in eight forest sites, ranging from undisturbed lowland sites to late secondary and exotic forest. Their study aimed to discover which site had higher numbers of bees. In addition, they wanted to investigate the bee habitat preference (i.e., vegetation structures and microclimates). The IDH was supported by Liow et al. (2001) as they reported that bee species richness and abundance in tropical lowland forests of Southeast Asia were highest in intermediate disturbance sites and lowest in undisturbed sites. The abundance of stingless bees increased as the number of big trees increased, and flower abundance increased with higher temperatures. The honey bee was not affected by the measured variables. Both *Lipotriches* and *Lasioglossum* abundance increased as flower intensity and temperature increased.

1.6. Restoration

Restoration allows new bee communities to establish in an ecosystem. The increase in abundance continues until a certain level is reached, then it begins to decline. This level is the carrying capacity, K, or the maximum capacity of a certain species in a habitat; this is where the birth rate is equal to the mortality rate (MacArthur & Wilson, 1967). Once a site has been reclaimed for restoration and disturbance is removed, the habitat undergoes stages of secondary succession and recovery. Disturbance levels start high and then gradually drop to lower levels (Simmons, 1999). Also, ecosystems react differently to disturbances due to the heterogeneity of each ecosystem (Fraterrigo & Rusak, 2008).

Toivanen et al. (2009) studied the effects of forest restoration treatments on the abundance of bark beetles in Norway spruce forests of southern Finland. Bark beetles are one of many species dependent on dead wood. The restoration of bark beetles used two methods: controlled burning and partial harvesting with down wood retention. They found that the number of bark beetles was positively affected by both treatments. When both of the treatments were used in the same area, the bark beetles reached their maximum abundance at treatment areas when compared with control areas. The restoration raised the resource accessibility, which increased bark beetles' abundance (Toivanen et al., 2009).

Steffan-Dewenter and Tscharntke (2001) investigated the succession of bee communities in southwest Germany. Three field types were studied, with four sites from each type: 1 year old fields with *Phacelia tanacetifolia*, 1- 5 year set-aside fields with naturally developed vegetation, and orchard meadows over 30 years old. They found that

bee communities changed as the vegetation changed. Also, the plant community exhibited major changes from being dominated by pioneer species to secondary succession stages, which is known to contain a high diversity stage. The changes in plant communities led to massive increases of bee abundance and diversity. The species richness of bees increased with succession age. The abundance of bees was higher in meadows, two year old set- aside fields and *Phacelia* fields. Bee abundance did not increase with succession age, but was strongly related to abundance of flowering plants. The species richness of bees correlated with the species richness of flower species. The soil nesting bees decreased with succession age, while above ground nesting bees increased (Steffan-Dewenter & Tscharntke, 2001).

Pollard (1975) studied the effects of forest open spaces on butterfly abundance during building of roads or paths in Monks Wood National Natural Reserve in England. Pollard's results agreed with Sparks et al. (1996) who investigated the effect of shade on plant species and butterflies in lowland woods in England and found that plant and butterfly abundance declined as shade increased. Waltz and Covington (2004) studied the effect of ponderosa pine restoration treatments in ponderosa pine and gamble oak forests located between Mt. Logan and Mt. Trumbull, USA. The results showed that restored sites had three to five times more butterflies in the treatment sites than control sites due to the greatest light intensity and plant diversity (Waltz & Covington, 2004).

1.6.1. Influence of restoration on community composition

Plant communities change during succession stages and result in changes in bee communities (Rao et al., 1990; Steffan-Dewenter & Tscharntke, 2001). Three factors influence the bee community patterns as a result of succession: colonisation ability,

habitat quality and biotic interactions (Steffan-Dewenter &Tscharntke, 2001). Nesting behaviour is one of many reasons for the changing of bee community composition. For example, soil nesting bees decline with succession age (Steffan-Dewenter & Tscharntke, 2001).

Bee community composition changes with time as a result of natural changes in the environment. The human use of land creates massive disturbances that radically transform environmental conditions that, in turn, affect and alter bee communities (Bommarco et al., 2011).

A number of studies specifically address the effect of habitat restoration on pollinators and examine how pollinator communities respond to restoration. Fiedler et al. (2012) investigated how the removal of an invasive plant, *Frangula alnus*, influenced bee, butterfly, and herbaceous plant abundance, diversity, and species composition. Bee abundance and diversity were influenced by restoration more than the plants. The abundance of bees was affected by removal treatment. The invaded plots had lower bee abundance than removal and reference plots, which were similar in the first year after restoration, but in the second year the removal plots had a higher abundance than the reference. The invaded plots had lower species richness in both years of study when compared to both removal and reference plots, which had the same level of species richness. This interpretation suggests that restoration increased bee abundance and diversity, and led to changes in the composition of communities (Fiedler et al., 2012).

The impacts of restoration on wild bees were studied in the inland sand dune grassland in northwestern Germany (Exeler et al., 2009). Two types of habitat and two treatments for each habitat type were used to investigate restoration effects on bee

community succession. The sites were restored sand grassland, restored sand dune, and two old natural reserve sites close to the restored sites in distance and vegetation coverage. The restoration was done by removing dykes and stopping cattle grazing, which created a new habitat. Bee communities changed rapidly in the few years following the restoration. The restoration affected both overall and specialized bee abundance, which had higher records within target sites, while parasitic bees were more abundant at the restored sites. Restoration had variable effects in different habitats. At the sand dune target sites, the overall abundance of specialist bees was higher than in restored sites, while generalists were more abundant in restored sites. In contrast, the sand grassland restoration sites and target sites had the same bee abundance. The specialist bee abundance was greater in restored sites while generalist bees were more abundant in target sites. The species richness of sand grassland increased with each year, but bee species richness in sand dunes was constant among years. The results confirm that in the few years following restoration, bee communities change rapidly. As a result, Exeler et al. (2009) concluded that bee species richness was the same in restored and target sites, but the abundance of bees was different between restored and target sites.

Williams (2011) searched for evidence that restoration actually improves community diversity by studying bee communities in restored sites along the Sacramento River channel in California. Mostly, the restoration programs focussed on target bees and ignored non-target bees. Bee and plant communities at restored riparian sites were compared to communities contained in the remnants of riparian habitat within the same region. Five sites of the same age (mid-succession) were sampled, each one hectare in size. Each site was twinned with nearby remnant riparian habitat of the same size. Bee

abundance and species richness were the same between the two types of sites. On the other hand, when bee communities' composition was taken into consideration, the two types of site were different in terms of relative abundance of bee species (Williams, 2011). In the end, restoration had an effect on bee abundance and species richness, since bee abundance and diversity increased in restored sites to the same levels of abundance and diversity at the control sites.

Hanula and Horn (2011) investigated the effects of removing Chinese privet from riparian forest in the Oconee on River watershed in northeast Georgia on bee abundance and diversity. The invasive shrubs affected the bee diversity and abundance negatively by reducing sunlight, lowering temperature, and impairing native plant growth. Removing the Chinese privet led to increased bee abundance and diversity. Mulched plots and plots where privet was felled had higher numbers of bees than the control plots. These results can be linked to the disturbance level because the mulched plots faced a greater amount of disturbance. There were positive relationships between the sunlight quantity and the plant coverage and the bee abundance, species richness, and diversity (Hanula & Horn, 2011).

1.7. Bees in restored landfill sites

Human landfill sites exemplify site disturbance, and there have been efforts to restore disturbed landfill sites in the Niagara region as a way to recover suitable habitats for supporting higher biodiversity (Richards et al. 2011). Restoration efforts mainly focus on remediating toxic environments, removing perturbations, returning disturbed ecosystem to natural functioning, and encouraging species diversity. The restoration work

in landfill sites can play an important role in achieving conservation goals (Rahman et al., 2011).

1.8. Carolinian Zone and Niagara Region

The Carolinian zone is located at the northernmost edge of the Eastern Deciduous Forest and limited to southwestern Ontario (Jalava et al., 2000; Meloche and Murphy, 2006). The Niagara escarpment runs through the Carolinian zone. Restoration becomes more valuable in the Carolinian zone because most of the natural cover was lost, while the remaining cover is highly disturbed by human activities. Restored landfills are patches of habitat that bees can inhabit and they provide ecological refuges to pollinators like bees through food and nesting resources (Richards et al., 2011; Roulston & Goodell, 2011). The Carolinian zone is highly disturbed by human activity and the natural cover forms just 15% (Jalava et al., 2000). The Carolinian zone is not big in size; it forms just 1% of Canadian land, but is rich in human population since 25% of Canadian residents live there (Kanter, 2005). The importance of the Carolinian zone must be acknowledged because one third of Canadian rare species reside there. Just 2% of the Carolinian zone is protected, while there is a high percentage of species at risk that inhabit unprotected areas (Meloche & Murphy, 2006). These examples highlight the need for restoration as a key role in species conservation.

The Carolinian zone has a wide range of habitat that is rich in biodiversity (Kanter, 2005; Riverie & Lawrence, 1999). The Carolinian life zone is high in biodiversity and hosts rare and unique endangered species (Allen et al., 1990). Also, it has unique species that are found nowhere else in the world (Kanter, 2005). The zone supports five bee families out of the six extant in North America (Richards et al., 2011).

1.8.1. Previous studies on Carolinian zone bee diversity

Grixti and Packer (2006) studied bee biodiversity north and east of the Niagara Escarpment in Ontario to investigate changes in wild bee communities as a result of short-term succession. They studied changes in bee community composition in one place over two time periods, 1968-1969 (MacKay & Knerer, 1979) and 2002-2003. Bees were sampled in 2003 and 2004 using the same method that MacKay and Knerer (1979) used in 1968 and 1969. In the first period the total number of bees collected was 9,784 individuals from six families, 26 genera, and 105 species. In period two, a total of 10,437 bees from six bee families, 27 genera, and 150 species were collected. A total of 15 bee species and 3 genera were restricted to period one. A total of 60 species and 4 genera were unique to period two. There were differences in bee relative abundance between periods one and two, even within common species across both periods, which represented 86% of both communities. Overall, bee species richness, diversity, and evenness were greater in period two than period one (Grixti & Packer, 2006). When the data from this study were examined using the randomisation program performed by Richardson and Richards (2008), the results disagreed with Grixti and Packer's conclusion that species richness was greater in period two. Species richness was fluctuating between years during both periods. Richards et al. (2011) study suggested that 2003 was a good year for bee abundance and diversity in many locations.

1.9. Previous research on bee diversity in Niagara

Richards et al. (2011) published a paper based on Rutgers-Kelly's (2005) research describing bee diversity in naturalizing patches of Carolinian grassland in southern Ontario. The main focus was bee patterns of recolonization within newly available

habitats. Bee communities were surveyed at sites representing different disturbance levels: low, intermediate, and high, in naturalizing meadow habitats in southern St. Catharines, Ontario, Canada.

The four low disturbance sites were located within the Brock University campus in St. Catharines. The intermediate disturbance sites, Escarpment and Residences, were located at the Glenridge Quarry Naturalization Site (GQNS). The high disturbance sites were Pond and St. David's which were also located at GQNS. Disturbance level and time since last disturbance were used to categorize each of the study sites. Brock University campus sites had lower abundance levels compared to GQNS sites. Specimens were collected using three different collection methods: pan traps, flower collections, and sweep nets. The biodiversity in each disturbance level was measured using species richness and abundance of individuals as gauges.

In Richards et al. (2011) 15,733 bee specimens belonging to five bee families (Halictidae, Colletidae, Andrenidae, Apidae, and Megachilidae) representing 124 species were collected, while abundance-based diversity estimators suggested 148 species. Moreover, Rutgers-Kelly (2005) she found that the low disturbance site had the most flower species (N = 17), followed by the intermediate level of disturbance (N = 15), followed by the high level of disturbance (N = 10). The conclusion was that in the intermediate sites, there were higher numbers of blooming flowers available for bees to forage on, which increased both the abundance and diversity of bees in these sites. Her study suggested that bee abundance and species richness are highly correlated. Also, she found that large size bees were more abundant in high disturbance sites than intermediate and low disturbance sites.

Rutgers-Kelly and Richards (2013) used a subset of the previous data of their 2011 study to investigated the effect of anthropogenic disturbance on the abundance and diversity of bees and investigate the patterns of bees in three regeneration levels: new, recent, and control. The new sites were newly planted meadows (age 0), the recent sites were three years old, while the control sites were more than 40 years old at the time of study (2003). Based on the Intermediate Disturbance Hypothesis and previous research done by Carvell (2002), they expected that the recent sites would be higher in abundance and diversity, followed by control sites, then new sites. The result of this study showed that bees were more abundant in recent sites, followed by control sites, then new sites. On the other hand, bee diversity was the highest in the recent sites (82 species), while it was almost the same in the new (67 species) and control levels (66 species).Rutgers-Kelly and Richards (2013) results were in agreement with the IDH. The intermediate level had the highest number of bees from each bee family. The low disturbance site had lower numbers of Apidae and Halictidae compared to Megachilidae, which was higher than expected. In the high disturbance site, lower numbers of bees were found for all bee families. Rutgers-Kelly and Richards (2013) suggested that newly restored habitats are inhabited immediately by bees, and it took up to 3 years to turn from pioneer communities to higher diverse communities with stronger competitors. Diversity and abundance then dropped over the next five to ten years. My study undertook to test the same bee community at some sites of Rutgers-Kelly and Richards' (2013) study in addition to newly restored landfills at two different locations.

León Cordero (2011) studied the same bee community as Rutgers-Kelly (2005) in terms of the annual variation in the phenology, abundance, and diversity during four

study years: 2003, 2004, 2006, and 2008. He classified bee species as abundant, common, or rare. He used bee specimens collected by pan traps only. His study was carried out at four sites located in GQNS and the Brock University campus, St. Catharines, Ontario. A total of 8,139 bee species belonging to 26 genera and subgenera, and at least 57 species were collected. The numbers of bees collected from the low disturbance sites Brock and BrockNW were higher than the bees collected from the high disturbance sites, Pond and St. David's. More rare and new species were found when the list of 2003 species was compared to other years. Also, his study supported the assertion that more abundant genera would occur consistently over years and would not switch to other abundance categories while common and rare species would change. This study showed the importance of restoration because it strongly supported that bee communities responded remarkably fast to changes in the ecosystem caused by disturbance. Therefore, bee assemblages are valued to indicate the biodiversity and the state of the ecosystem (Duelli & Obrist, 1998; Kevan, 1999). Quintero et al. (2010) stated that the composition of bee species positively correlated with habitat change caused by anthropogenic disturbance.

1.10. Objectives and hypotheses

My research focuses on the initial two years of restoration in restored landfill sites. This work highlights the role of landfill site restoration in creating new habitats that can be recolonized in areas where bees had been eliminated. Bee abundance and diversity is compared between new restoration sites, old restoration sites, and control sites to observe the establishment of bee communities in new habitats after massive disturbance.

Based on the Increased Disturbance Hypothesis (InDH) and the Intermediate Disturbance Hypothesis (IDH), I predicted two patterns of bee abundance. The first

pattern, which is based on the IDH, is that bee abundance will increase dramatically when a short period of time has passed since the last disturbance because new niches are available to species to colonize, increased resources are available, and competition is limited. According to León Cordero's established patterns in bee abundance and diversity, I expect to see that bee abundance will be higher in disturbed sites than control sites since I am testing the similar bee community. The second pattern, based on the InDH, is that newly restored sites will show the lowest numbers of bees, while increases in abundance will occur in old restoration sites, but the maximum level of abundance will occur at the control site (Figure 1.1a). Based on the intermediate disturbance hypothesis, I expected to see the highest abundance at the old restoration sites, followed by the control sites, followed by newly restored sites (Figure 1.1b).

Regarding bee diversity, according to InDH, I predict that control sites will display ever-increasing levels of species richness as time passes. This means that the control site, Brock South, should have the highest species richness followed by the old restoration sites, Pond and Escarpment, then the newly restored sites Em1, Em2, and Station Road (Figure 1.2a). The second expectation is based on the IDH, which predicts that the greatest species richness will be displayed at an intermediate time after recovery. Previous studies have shown that bee species richness increased for at least three years (Rutgers-Kelly & Richards, 2013). I expect to find the highest bee diversity at the old restoration sites, Pond and Residence, which represent the intermediate level of disturbance, followed by the control and newly restored sites (Figure 1.2b).

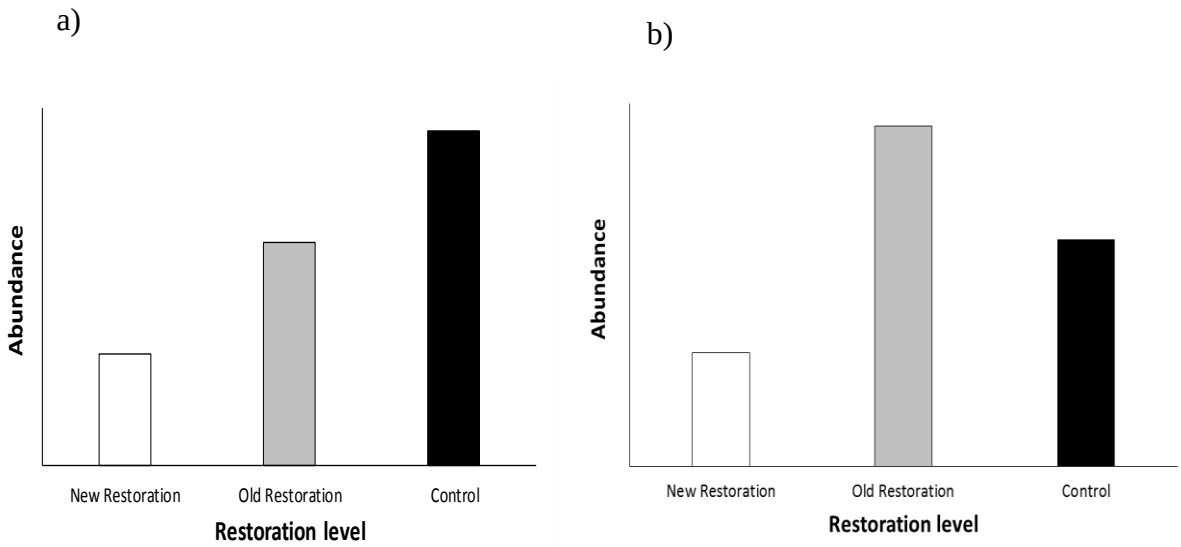
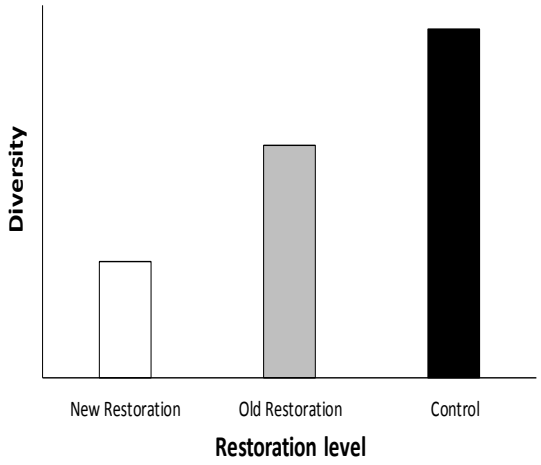


Figure 1.1. The two expected patterns of change in bee abundance among different restoration levels. a) The Increased Disturbance Hypothesis (InDH) which shows increased abundance as the disturbance decreases with restoration time. b) The Intermediate Disturbance Hypothesis (IDH) which shows greater abundance at the intermediate level of disturbance at the old restoration sites followed by the control then the newly restored site. Restoration level refers to the time since the last major disturbance.

a)



b)

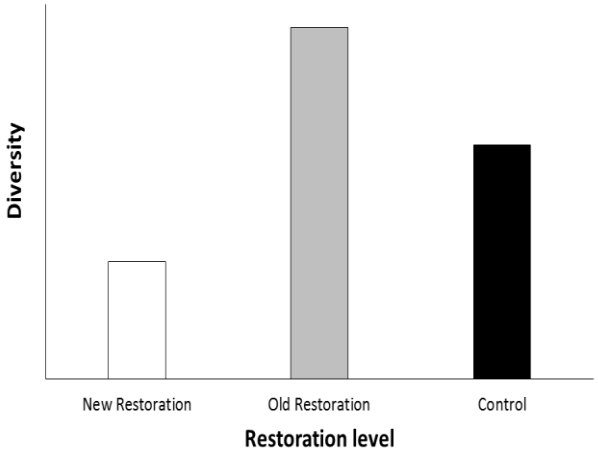


Figure 1.2. The two expected patterns of change in bee diversity among different restoration levels. a) The Increased Disturbance Hypothesis (InDH) which shows increased diversity as the disturbance decreases with restoration time. b) The Intermediate Disturbance Hypothesis (IDH) which shows greater diversity at the intermediate level of disturbance at the old restoration sites followed by the control then the newly restored site. Restoration level refers to the time since the last major disturbance.

2. MATERIALS AND METHODS

2.1. Sampling locations

Bee abundance and diversity were examined in the meadows of restored landfill sites. All study sites were located in three cities in the Niagara Region of southern Ontario, Canada: St. Catharines, Port Colborne, and Wainfleet (Figure 2.1).

The first site sampled was Brock South (BrS, Figure 2.2) on the campus of Brock University in St. Catharines in southern Ontario (latitude: N 43º06.733', longitude: W 79º14.781'). Brock South is now a meadow after being used as farmland until the1960s. BrS was chosen as a control site because bees were presumed to already be there compared to other sites where vegetation was not available until restoration. BrS is vegetated primarily by grass and wildflowers.

Two sites were sampled in the Glenridge Quarry Naturalization Site (GQNS) adjacent to Brock University (Figure 2.3). Pond was named according to its location on the slope near the pond in the GQNS (latitude: N 43º07.436', longitude: W 79º14.205'). The second site was named Escarpment as it was placed near the edge of the escarpment (latitude: N 43º07.406', longitude: W 79º14.239'). The Escarpment site was a large area of grass with patches of wildflowers. One transect was placed at the Pond site, and the other transect was placed on the Escarpment.

The GQNS was used intensively as farmland until the 1960s when it was turned into a limestone quarry. After being a quarry, it became a municipal landfill from November 1976 to December 2001 when the site was closed and restoration work began in 2003. GQNS is a mix of meadow with woodland edges. GQNS was chosen because it represents old restored sites prior to 2011.

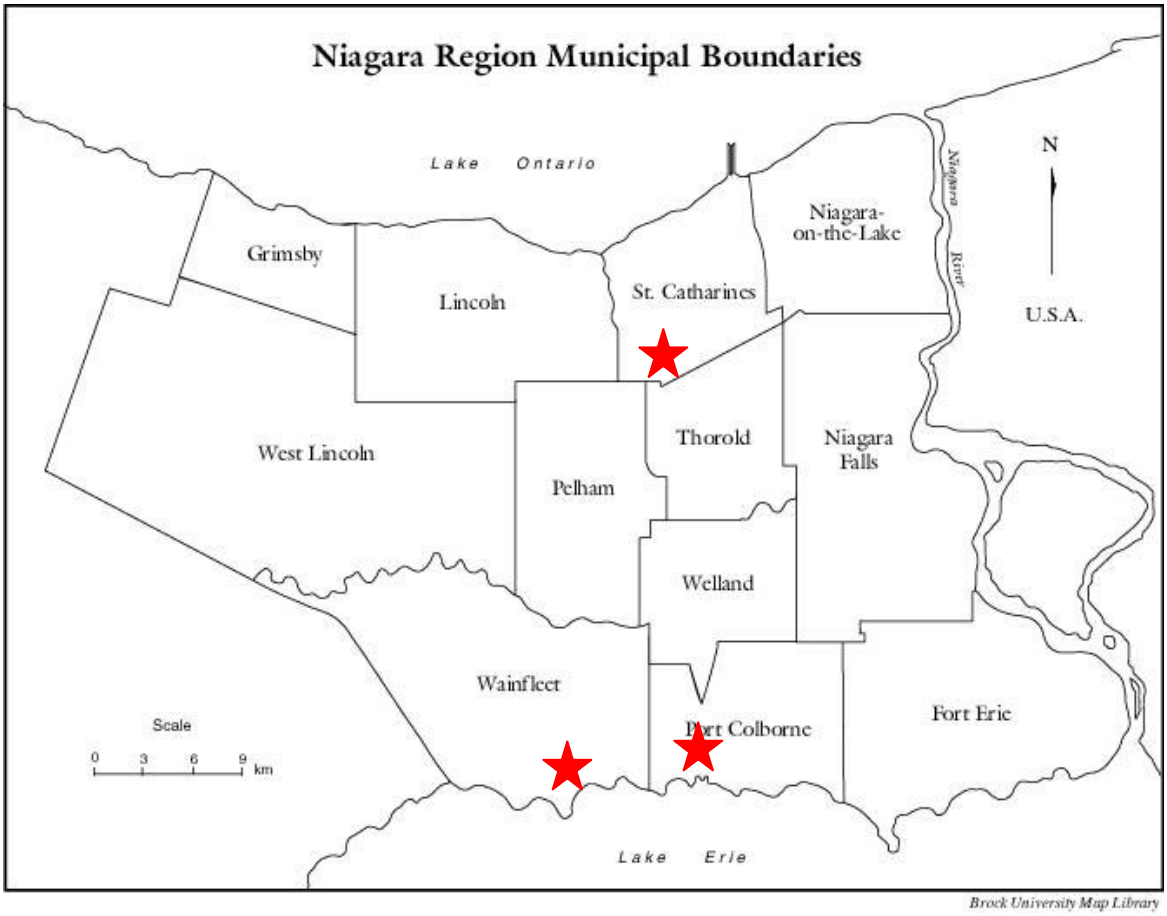


Figure 2.1. Locations of study sites in St. Catharines, Port Colborne, and Wainfleet, Ontario, Canada. St. Catharines included three sites: Brock South, Pond, and Escarpment. Port Colborne includes two sites: Em1, Em2. Wainfleet included one site, which is Station Road. (Brock University Map Library, 2011).

Figure 2.2. a) An aerial view showing the location of first study site Brock South, in St. Catharines, Ontario (Google Maps, 2013). b) The arrows showing the location of the pan trap transect (Niagara Navigator, 2011).

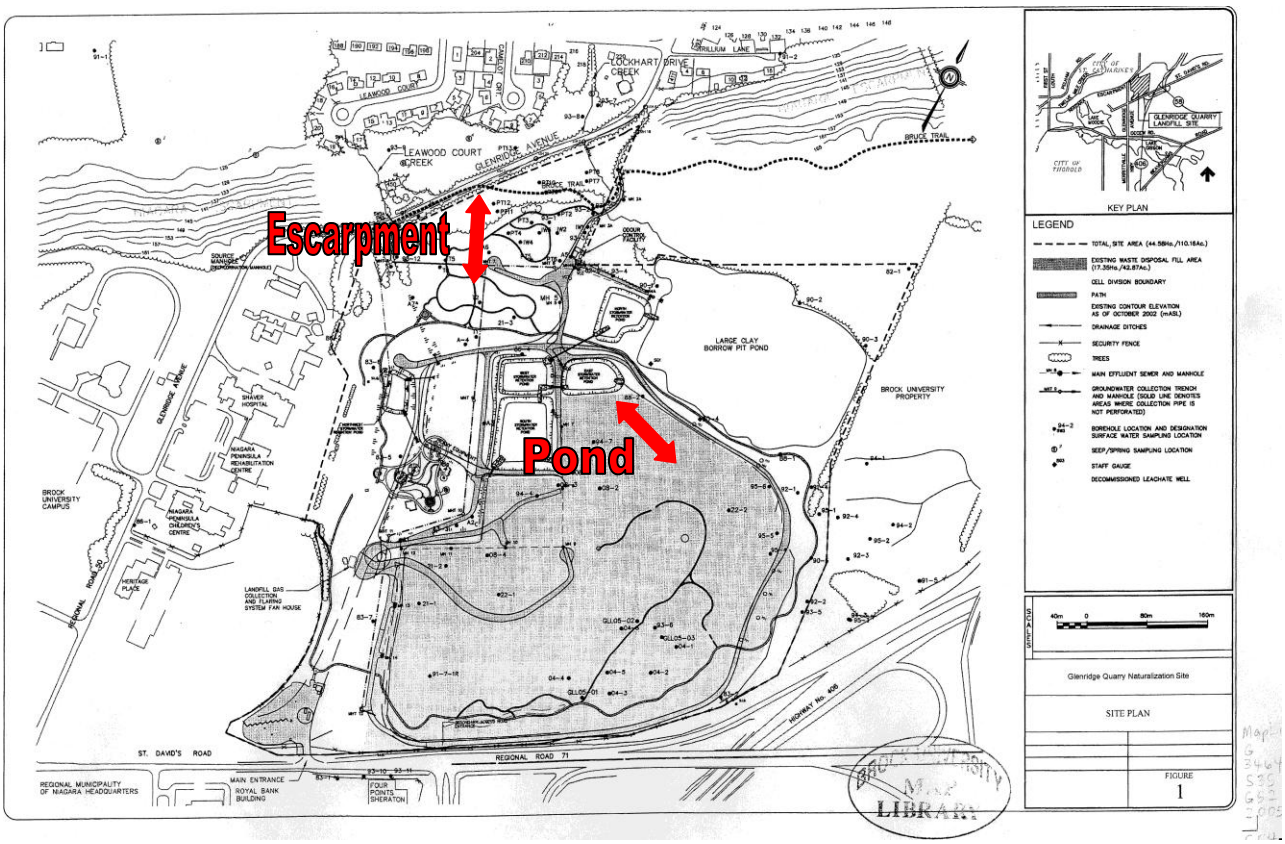


Figure 2.3. Glenridge Quarry Naturalization site map (GQNS), in St. Catharines, Ontario, showing the two pan trap transects Pond and Escarpment (Brock University Map Library, 2005).

In 2003, the Pond site was in its first year of restoration, while the Escarpment site, restored in 2000, was in its third year of restoration. The Pond site in 2003 was equivalent to the newly restored sites Em1, Em2, and Station Road in 2011.

Two sites were sampled at the Elm Street Naturalization Site in Port Colborne, Ontario. The site size is approximately 0.5 km^2 and was used for domestic and commercial solid waste, brush, and construction debris from the 1950s until 2009. In 2009, composting operations were terminated and in 2010, the site was closed and covered. Entire planting of the site was completed in 2011. Two pan trap transects were placed at the Elm Street site, and they are called Em1 (latitude: N 42º54.345', longitude: W 79º15.180') and Em2 (latitude: N 42º90.025', longitude: W 79º25.554') (Figure 2.4). The Em sites are a mix of naturalization area, meadow, and pond, where native plants and flowers thrive. The Elm Street site was chosen because it represented newly restored landfills.

The last site was located at the Station Road Naturalization Site (StR) in Wainfleet, Ontario (latitude: N 42º54.612', longitude: W 79º22.394'). The size of the site is 73,000 m^2 (approximately 0.07km^2). Station Road was used as a municipal landfill site from the 1950s to 2008. One transect was placed in StR (Figure 2.5). StR is a mix of ponds, wooded area and naturalization area. StR was chosen because it was a newly restored landfill site in 2011.

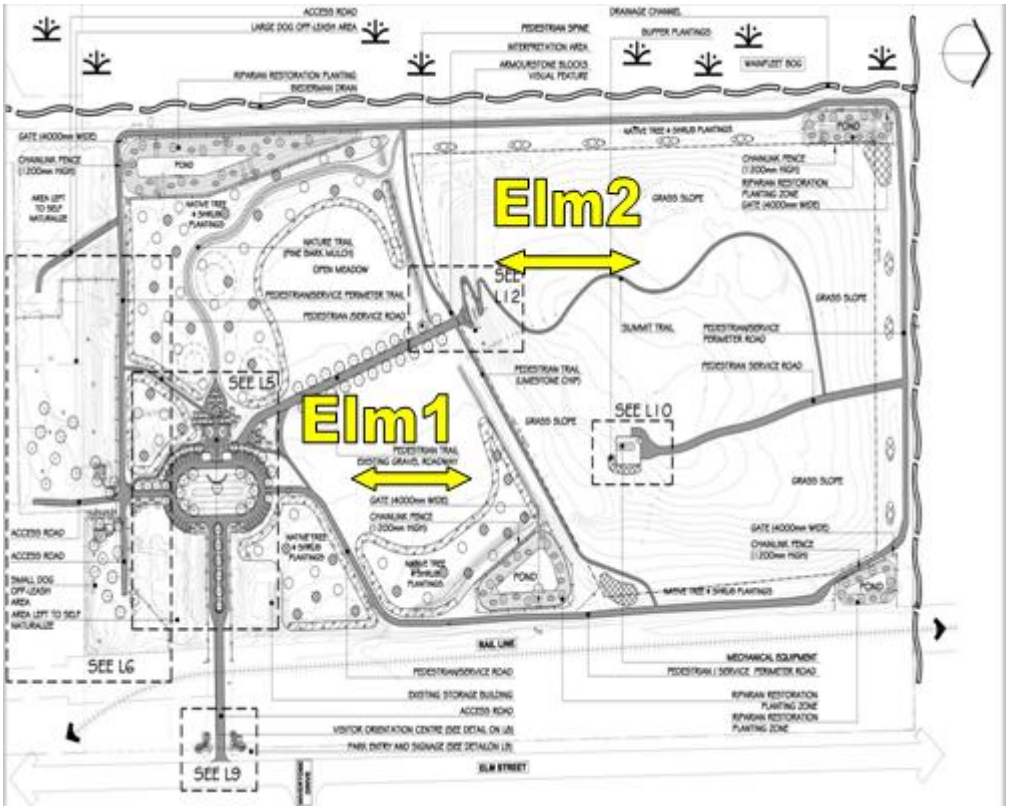


Figure 2.4. Elm Street site, Port Colborne, Ontario, with the two transects Em1 and Em2. (Niagara Region, 2009)

Figure 2.5. Station Road site, Wainfleet, Ontario showing the pan trap transect (Niagara Region, 2009).

2.2. Bee collections

Bees were collected using pan trapping and netting from flowers (flower collection). The standardized NSERC-Canadian Pollinator Initiative (CANPOLIN) sampling protocol was used to collect project data (NSERC-CANPOLIN, 2009). In 2011, the field season began in the week of 25 May and ended 10 October. In 2012 the field season began in the week of 22 March and ended 20 September. Sites were sampled approximately biweekly. The two-week period allows enough time for all sites to be sampled without weather complications. Weeks were numbered from the usual first week of the spring season, which started May 1st, until the last week of the summer season, which ended at the end of October (Richards et al. 2011).

2.2.1. Pan trap collection

In 2011, pan trap collections started 25 May (Week 4) and ended 10 October (Week 24), while in 2012 pan trap collections started 22 March (Week 4) and ended 20 September, 2012 (Week 22) (Appendix 2.1). Pans were placed out in the morning before 9:00 a.m. and collected after 3:00 p.m. Samples were taken on warm, calm, sunny days, since the cold, windy, and rainy days decreased the foraging activities of bees so in 2011 sampling did not happen in weeks 0-4 until the rain stop but in 2012 the sampling start earlier because the temperature start to rise and bees activities start to be noticeable. Traps were plastic bowls (SOLO PS6-0099, 6 oz.). Thirty bowls were placed along a straight transect 87m in length, alternating between yellow, white, and blue, 10 traps of each colour (white, the original colours of bowls; fluorescent yellow Krylon paint #3104; and fluorescent blue #3109). Different colours were used to attract different types of bees. The distance between the pans was 3m as required per the CANPOLIN protocol

(NSERC-CANPOLIN, 2009). Traps were filled ¾ full with soapy water (5 drops of blue Dawn dish detergent per litre of water). The bees that landed on the water surface drowned. Pan trap contents were poured into a strainer, and specimens were stored in plastic containers labeled with the trap colour, date, and site name. Samples were taken to the laboratory where they were rinsed with tap water. Specimens were stored in plastic bags (Nasco Whirl-pak) filled with 70% ethanol and labeled with date, site name, and colour of pans.

2.2.2. Flower collections

The flower collections sites were the same as the pan trap sites except for the old restoration level where the two sites were companied to one big sites called GQNS. The flower collections were done at each of the restoration levels as the following: **BrS** which represented the control level, **GQNS** which pool the two old restoration sites Pon and Esc and represented the old restoration level, and **Em1, Em2, StR** which represented the new restoration level. Flower collections were started in week 6 when there were large enough patches of flowers. Depending on the weather, flower collections were done on the same day as pan trapping or the day after. Bees were collected using nets (folding collapsible insect nets, Bioquip 7112CP: 30 cm diameter, 12.7 cm aluminum handles). Flower collections were done in all sites alternating between morning and afternoon. For each collection, I chose a patch of the same flower type big enough to be sampled for 5 minutes without sampling the same blossoms twice. The flower species patch was sampled by setting a timer for 5 minutes. The flower collection was done by catching every bee visible in the patch. An orange flag was placed at the start point, and another orange flag identified the end point. A tape measure was used to measure the distance

between the start point and the end point to measure the patch size. Specimens were stored in 50 ml Falcon tubes (Fisher Brand) filled half full with 70% ethanol and labeled with the date, site, flower name, and patch size. A flower from each patch was collected and identified using the ROM Field Guide to Wildflowers of Ontario (Dickinson et al., 2004) (Appendix 2.2).

2.3. Identification of specimens

Specimens were first separated into bees and non-bees. Bees were dried on paper towel, with larger bees being dried by fluffing with pressurized air. Labels were printed on acid free, 100% linen ledger #36 white papers with site, initials of collector, date, collection method, flower ID, and patch size indicated. Bees from all sites were pinned using insect pins (Austerliz insect pins: Black Enameled). Depending on the size of the bees, different sizes of pins were used (size 0, 1, and 2).

Bee specimens were identified using identification guides (Gibbs, 2010, 2011; Laverty & Harder, 1988; Michener, McGinley & Danforth, 1994; Mitchell, 1960, 1962), for *Dialictus*, and Rehan and Sheffield (2011) for *Ceratina*, and the online guide Discover Life for identification of bees of eastern North America (http://www.discoverlife.org/mp/209) (Packer et al., 2007). Bees were identified by Rola Kutby, Thomas Onuferko, Cory Sheffield and Jason Gibbs. Specimens were data based in Microsoft® Excel 2007.

Andrenidae family specimens were removed from all data analyses. Most of Andrenidae bees belonged to *Andrena* genus. *Andrena* is a very diverse species which makes identification to species level very difficult.

2.4. Data analysis

2.4.1. Community temporal variation

The temporal variation was studied to show whether the number of bees collected in spring (Weeks -4 to 11) differed significantly from the number of bees collected in summer (Weeks 13 to 24), in both 2011 and 2012. The null hypothesis is that the number of bees collected over the flight seasons has an even distribution.

2.4.2. Abundance

Data analysis of abundance and family patterns in different levels of restoration

Em1 and Em2 sites were geographically near one another; both were located at the Elm Street Naturalization site and bees collected from these two sites were expected to represent the same bee community. I do not, however, expect them to be the same because they are ecologically different and I also observed a clear difference in the vegetation coverage at these two sites.

Analysis of variance using General Linear Model (GLM) was used in R studio v0.97 with significance $p < 0.05$. Bees were used to test if there was any difference in bee abundance caused by site effects. The linear model did not find a site difference, but in 2011, it is very clear that until about week 16, there were far fewer bees in Em2. In fact, there was a big difference in the vegetation, and Em2 had to be replanted in midsummer of 2011. Therefore, Em1 and Em2 are quite different ecologically, if not statistically, so they cannot be pooled. As a result, just the data from Em2 was used.

The large number of bees which were sampled in the study suggests that with the large sample size the normal or log-normal distribution is not expected. Log abundance was used in the model. The log transformation makes the non-normal distributed data more normal.

General linear models were performed to test the effect of the explanatory variables: biweekly collection period, year, family, species, and site under restoration level, on the response variable, and bee abundance, which was measured as the number of bees collected per week per site per morphospecies. A biweekly collection period has a major effect on variation in bee abundance (Richards et al. 2013), so it was consistently the first variable in all models. This allowed me to see if there were still significant restoration and site effects, which are the main interest of this research after variation among collection periods and species has been accounted for. The model was as follows: Log (Abundance) ~ Biweekly collection period + Family (Species) + Year + Restoration level (Site). The variation in bee abundance was studied for each family and determined separately by performing GLM tests.

2.4.3. Bee diversity

Data analyses of species of 2011 and 2012

I measured bee diversity as species richness. As more individuals are collected, more species could be recorded (Richardson and Richards, 2008). Splitting the effect of abundance from the species richness is important to make sure that the differences in diversity were due to the differences in species richness, not due to differences in abundance since I had unequal numbers of sites in each of the restoration levels. For example, the old restored level had twice as many sites as the control level, but species richness may not be double. To determine if species richness was different between the restoration levels both randomisation and rarefaction analyses were used.

Randomisation to compare species richness

The randomisation analyses were used to test the null hypothesis, which holds that species richness was the same among restoration levels. The software (Richardson and Richards, 2008) randomly dispenses each bee to each restoration level with regard to the number of bees from each species, and the number of bees collected in each restoration level. This procedure was repeated 10,000 times and generated a frequency distribution of the expected species richness. The mean, standard deviation, and the confidence interval of the generated frequency distributions were calculated in Excel. The observed species richness values for 2011 and 2012 were compared to the confidence interval foe the expected frequency distribution to identify significant differences among the restoration levels. When the observed species richness values fell within the confidence interval of frequency distribution, there were no significant differences between the observed number of species and the mean expected number of species. On the other hand, when the observed number of species fell outside the confidence interval of frequency distribution, there were significant differences between the observed number of species and the mean expected species.

Twenty-two specimens belonging to the subgenus *L. (Dialictus)* were removed from the species list of 2011 because they were badly damaged and unidentifiable to species level. Four specimens belonging to the subgenus *L. (Dialictus)* and one belonging to *Bombus* were removed from the 2012 analysis because they were badly damaged and unidentifiable to species level.

Rarefaction curve to compare species richness

For both years, the new restoration sites were higher in species richness than the control and old restoration sites. Using individuals-based rarefaction species richness can

be compared when the sampling effort is different. It is expected that greater sampling effort would yield a larger sample and more species, so species richness cannot be compared until the sample effort is equal among restoration levels. Rarefaction curves were performed to compare species richness among restoration levels using the Rarefaction Calculator software (Krebs & Brzustowski, 2000). Rarefaction was used to estimate species richness based on the smallest sample size. The software estimator gives the correct values for the true richness based on the set of samples.

Rank abundance

Rank abundance plots rank species according to their abundance. The shapes of curves are used to obtain detailed information about community structures. The sharp slope of a curve means a higher degree of dominance, while a soft slope means a lower degree of dominance (Murry et al., 1999).

2.4.4. Flower collections

Bees collected on flowers were studied separately for 2011 and 2012, as the flower abundance and diversity changed with time since restoration (Weiner et al., 2011; Beckage and stout, 2000; Lavorel et al., 1999). The flowers were sampled based on the availability of blossoms. The total numbers of bee collections in each restoration level were based on five minute sampling. Bees were collected from 20 different species of wildflowers. The availability of each flower was measured as the total number of flower collections at each site. The abundance of bees was divided by the number of samples for each flower species. The number of bees per sample in each site is divided by the total number of bees over the number of samples. The result is then compared with the number of bees per sample among restoration levels. The new restoration level had three sites, so

the mean number of bees of the three sites was used. Attractiveness to bees of each flower species was calculated as the number of bees on flower species divided by the number of samples taken from that flower species. Preference was calculated as the absolute preference for each plant divided by the number of individuals.

3. Results

3.1. Description of the bee community

3.1.1. General description of the structure of the bee community in restored landfill sites

A total of 4,023 bees were collected using only pan traps in 2011 and 2012 (Table 3.1.). Specimens belonged to five families (Apidae, Andrenidae, Colletidae, Halictidae, and Megachilidae), 25 genera and subgenera, and at least 80 species (Table 3.1). The most abundant families were Halictidae and Apidae, followed by Megachilidae, Colletidae, and Andrenidae. The families Halictidae, Apidae, and Megachilidae were the highest in generic richness with 7 genera. The number of bees varied among families (Figure 3.1), thus rejecting the null hypothesis that bee specimens were equally distributed among families (Goodness of fit test, $\chi^2 = 4708.4$, $d.f. = 4$, $p < 0.0001$).

Halictidae was the highest abundance with 2,546 bees, which comprised 61.4% of all bees collected. Andrenidae were lowest in abundance with 34 specimens which comprised 0.8% of the bee abundance (Figure 3.1). The family Colletidae was the lowest in generic richness with 1 genus, followed by Andrenidae which had 2 genera. Of the 81 species collected, 19 were represented by a single individual. The most abundant genus was *L. (Dialictus)* which comprised 32% of all bees collected, followed by *Augochlorella*, which comprised 21% of the sampled individuals. Halictidae was the most abundant family while the Andrenidae had the lowest abundance in both years (Figure 3.1). The family Colletidae was the lowest in generic richness with 1 genus, followed by Andrenidae which had 2 genera. Of the 81 species collected, 19 were represented by only a single individual. The most abundant genus was *L. (Dialictus)*

Table 3.1. Complete list of specimens captured and identified from pan traps in 2011 and 2012 from six sites, Brock South (BrS) at Brock University, Pond (Pon), and Escarpment (Esc) at Glenridge Quarry Naturalization Site in St. Catharines, Elm1 (Em1) and Elm 2 (Em2) sites at the Elm Street Naturalization Site in Port Colborne, and Station (StR) at Wainfleet, Ontario.

Family	Genus and subgenus	Species and Author	Control	Old Restoration		New Restoration			
			BrS	Pon	Esc	Em1	Em2	StR	Total
Andrenidae	*Andrena*	*carlini* Cockerell	1						1
		cressonii Robertson	3						3
		erigeniae Robertson		1	1			1	3
		nasonii Robertson	1		3				4
		vicina Smith						1	1
		sp.	6	5	6	1	3		21
	Calliopsis	sp.						1	1
Andrenidae Total			11	6	10	1	3	3	34
Apidae	*Anthophora*	*bomboides* Kirby						1	1
		terminalis Cresson					1	1	2
	Apis	*mellifera* L.	11	15	19	17	8	9	79
	Bombus	*bimaculatus* Cresson	1	1		1			3
		borealis Kirby		1		1			2
		fervidus Fabricius				2			2
		griseocollis (DeGeer)	5	6				1	12
		impatiens Cresson		4	5	4	3	1	17
		rufocinctus Cresson	2	3	1	1	1	3	11
		sandersoni Fkln.		1					1
		terricola Kirby	1						1
		unidentifiable						1	1
	Ceratina	*calcarata* Smith	37	17	33	11	19		117
		dupla L.	24		2				26
		dupla/mikmaqi	64	29	37	66	37	4	237
		mikmaqi Rehan & Sheffield	67	48	18	14	10	2	159
	Melissodes	*desponsa* Smith						2	2
		druriella Kirby		2					2

Table 3.1. (Continued)

Table 3.1. (Continued)

Family	Genus and subgenus	Species and Author	Control	Old Restoration		New Restoration			
			BrS	Pon	Esc	Em1	Em2	StR	Total
	Nomada	*bidentate* Cockerell			1				1
	Xylocopa	*virginica* (L.)				1			1
Apidae Total			212	127	116	118	79	25	677
Colletidae	*Hylaeus*	*affinis* Smith	75	32	17	26	31	11	192
		affinis/modestus	2		1	1	2		6
		annulatus (L.)	1			3			4
		hyalinatus Smith		1				2	3
		mesillae Cockerell		1			2		3
		modestus Say	29	2	4	5	1	5	46
Colletidae Total			107	36	22	35	36	18	254
Halictidae	*Agapostemon*	*virescens* (F.)	2	9	3	1			15
	Augochlora	*pura* Say	2	3	1	1	1	2	10
	Augochlorella	*aurata* Smith	184	264	215	72	114	25	874
	Halictus	*confusus* Smith	13	10	11	12	8	21	75
		ligatus Say	47	14	17	11	6	33	128
		rubicundus Christ	4			1	1	2	8
	Lasioglossum	*admirandum* Sandhouse	60	41	36	14	15	14	180
	(Dialictus)	*atwoodi* Gibbs	4			1	2	1	8
		cressonii Robertson	3	1				1	5
		ellisiae Sandhouse		1					1
		ephialtum Gibbs	2	4		1		4	11
		fattigi Mitchell	1	2		4	1		8
		hitchensi Gibbs	37	13	9	168	129	324	680
		imitatum Smith	12	2			1	3	18
		laevissimum Smith		2	1	4	3	19	29

Table 3.1. (Continued)

Family	Genus and subgenus	Species and Author	Control	Old Restoration		New Restoration			Total
			BrS	Pon	Esc	Em1	Em2	StR	
		leucocomum Lovell						1	1
		lineatulum Crawford	1		1			1	3
		hitchens Gibbs	37	13	9	168	129	324	680
		nigroviride Graenicher				1			1
		nymphaearum Robertson	4	2					6
		oblongum Lovell				1	1	6	8
		paradmirandum Knerer & Atwood	3	1		57	11	24	96
		perpunctatum Ellis	1		1	2			4
		pilosum Smith						2	2
		sagax Sandhouse				1			1
		Versatum Robertson	52	13	4	18	18	92	197
		viridatum Lovell	2	1				3	6
		weemsi Mitchell		2	1		2	1	6
		zephyrum Smith			1	1		1	3
		unidentifiable	3	1	3	11	2	6	26
	Lasiglossum (Lasioglossum)	*leucozonium* Schrank	8	3		5	3	18	37
		zonulum Smith	2		3	4	7	61	77
		coriaceum Robertson		3	2	6	7		18
	Lasiglossum (Evylaeus)	*cinctipes* Provancher	1						1
	Sphecodes	*atlantis* Mitchell		1			1		2
		dichrous Smith	1						1
Halictidae Total			449	393	309	397	333	665	2546

Table 3.1. (Continued)

Family	Genus and subgenus	Species and Author	Control	Old Restoration		New Restoration			Total
			BrS	Pon	Esc	Em1	Em2	StR	
Megachilidae	*Anthidium*	*manicatum* (L.)	1	19	10	2		2	34
		oblongatum lliger	1	1					2
	Coelioxys	*Octodentata* Say				2	1	2	5
		rufitarsis Smith		1	2				3
	Heriades	carinatus Cresson			1				1
									1
		leavitti Crawford	1						1
		variolosa Cresson		1					1
	Hoplitis	*pilosifrons* Cresson	3	2	1		2	1	9
		producta Cresson			3				3
		spoliata Provancher	2	1	8				11
	Megachile	*brevis* Say	4	5	14	16	10	10	59
		campanulae Kirby			1				1
		ericetorum Lepeletier			1		1		2
		latimanus Say						1	1
		mendica Cresson						1	1
		pugnata Say	1						1
		relativa Cresson		1				1	2
		rotundata (F.)		1	4	1	1	1	8
	Osmia	*atriventris* Cresson	2		1	5	5		13
		conjuncta Cresson	64	65	183	5	5	2	324
		pumila Cresson	12	7	2	3	1	2	27
	Stelis	*lateralis* Cresson	2					1	3
Megachilidae Total			93	104	231	34	28	22	512
Grand Total			873	666	688	584	479	733	4023

which comprised 23% of all bees collected followed by Augochlorella, which comprised 21% of the sampled individuals. Halictidae was the most abundant family and the Andrenidae had the least abundance in both years (Figure 3.1).

3.1.2. Description of the bee communities of the three restoration levels and their respective sites

My study sites represented three restoration levels. Brock South represented the control level, Pond and Escarpment sites represented old restoration level, and the Em1, Em2 and Station Road sites represented the new restoration level.

Control site

- **Brock South**

I caught 873 bees from 19 genera and 48 species from the control site Brock South over the two years (Table 3.1). Bees were classified into five families: Apidae, Andrenidae, Colletidae, Halictidae, and Megachilidae. The family Halictidae was the most abundant with 449 specimens, which comprised 51% of all specimens. The family Andrenidae had the lowest abundance with 11 individuals, which comprised 0.1% of all individuals. The most abundant genus was *Ceratina* with 192 specimens. The most abundant species was *Augochlorella aurata* with 184 specimens.

Old Restoration Sites

- **Pond**

I collected 666 bees from the old restoration site Pond. The bees belonged to five families, 19 genera, and 45 species (Table 3.1). The family Halictidae was the most abundant with 393 specimens, comprising 59% of all individuals. The family Andrenidae

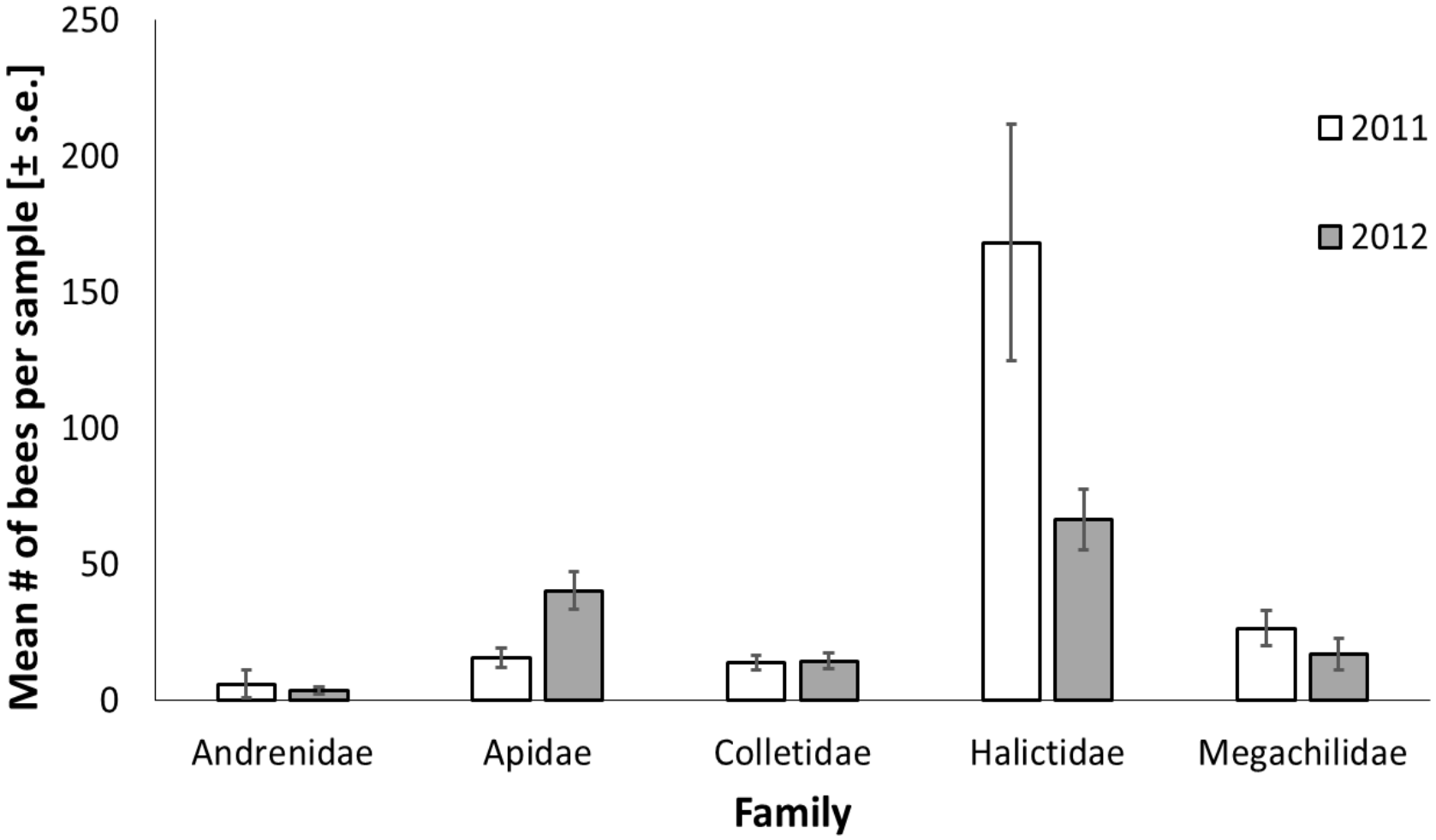


Figure 3.1. The distribution of the mean number of bees per sample among bee families for both study years. The Halictidae had the highest abundance while the Andrenidae had the lowest abundance in both years.

had the lowest abundance with 6 individuals. The most abundant genus and species was *Augochlorella aurata* with 264 specimens.

- **Escarpment**

I collected 688 bees from the Escarpment site. The bees belonged to five families, 18 genera, and 36 species (Table 3.1). The family Halictidae had the most abundance with 309 specimens, comprising 45% of all individuals. The family Andrenidae had the lowest abundance with 10 individuals, which comprised 0.1%. The most abundant species was *Augochlorella aurata* with 215 specimens.

Newly Restored Site

- **Em1**

A total of 585 bees were collected from the restored site, Em1. Bees belonged to five families, 16 genera, and 40 species (Table 3.1). The most abundant family was Halictidae with 397 individuals, which comprised 68% of all individuals collected. The lowest abundance family was Andrenidae with 1 individual collected. The most abundant genus was *L.* (*Dialictus)* with 285 specimens, and the most abundant species was *L. (Dialictus) mitchelli* with 168 specimens.

- **Em2**

I collected 479 bees from the newly restored site, Em2. The bees belonged to five families, 16 genera, and 32 species over the years (Table 3.1). The family Halictidae had the most abundance with 333 specimens, comprising 69% of all individuals. The family Andrenidae had the lowest abundance with 3 individuals. The most abundant subgenus was *Lasioglossum* (*Dialictus)* with 185 specimens. The most abundant species was *L. (Dialictus) mitchelli* with 129 specimens.

- **Station Road**

I caught 733 bees from 19 genera and 43 species from the newly restored site, Station Road (Table 3.1). Bees were classified to the five families. The family Halictidae had the most abundance with 665 specimens, comprising 90% of all individuals. The family Andrenidae had the lowest abundance with 3 individuals. The most abundant subgenus and species was *L. (Dialictus) mitchelli* with 503 specimens.

3.2. Community temporal variation

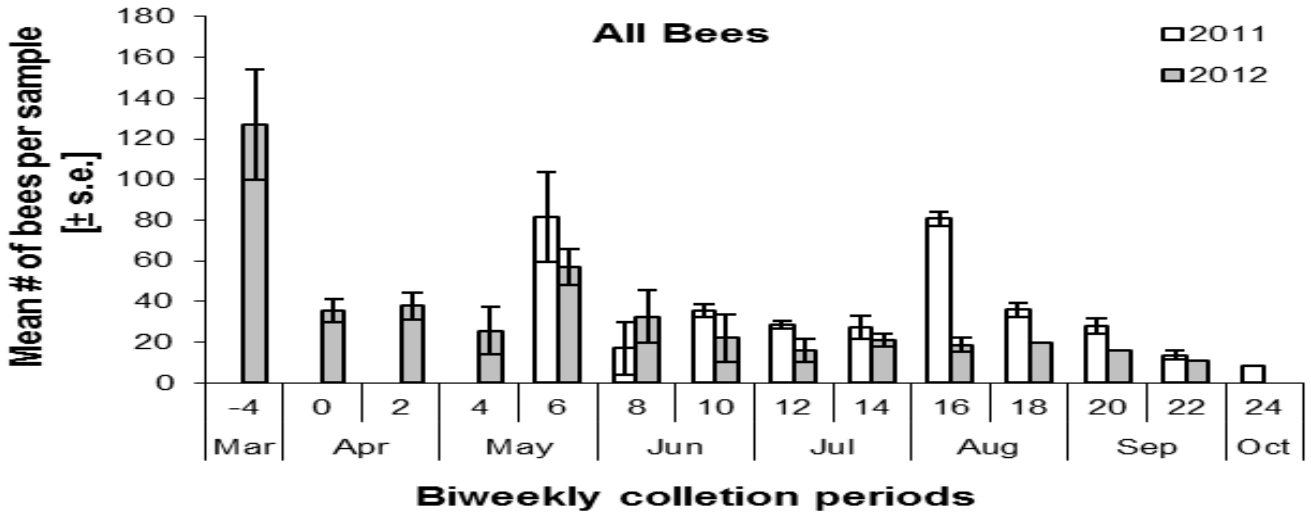
3.2.1. Abundance peaks of restored landfill bee communities

In 2011, there were two peaks of bee abundance (Figure 3.2a). The first peak occurred in the spring (week 6 in the end of May), and the second peak was in the summer (week 16 in the beginning of August). There was a decline in the number of bees collected between weeks 8 and 14, and between weeks 18 and 22. Figure 3.2a showed that there were two distinct bee seasons in 2011: spring (week 6 to the week 8) and summer (week 16 to week 18).

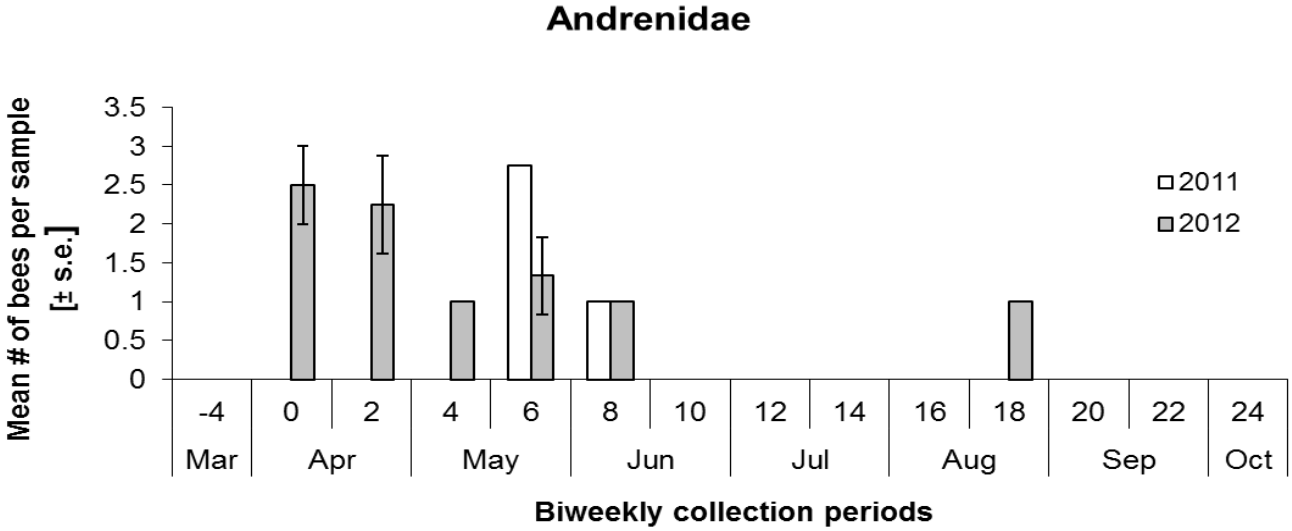
In 2012, bees were very abundant and were first collected at the end of March (week -4) with a second peak at the end of May (week 6). There was a decline in the number of bees collected after week 6 until the end of the collection season in week 24.

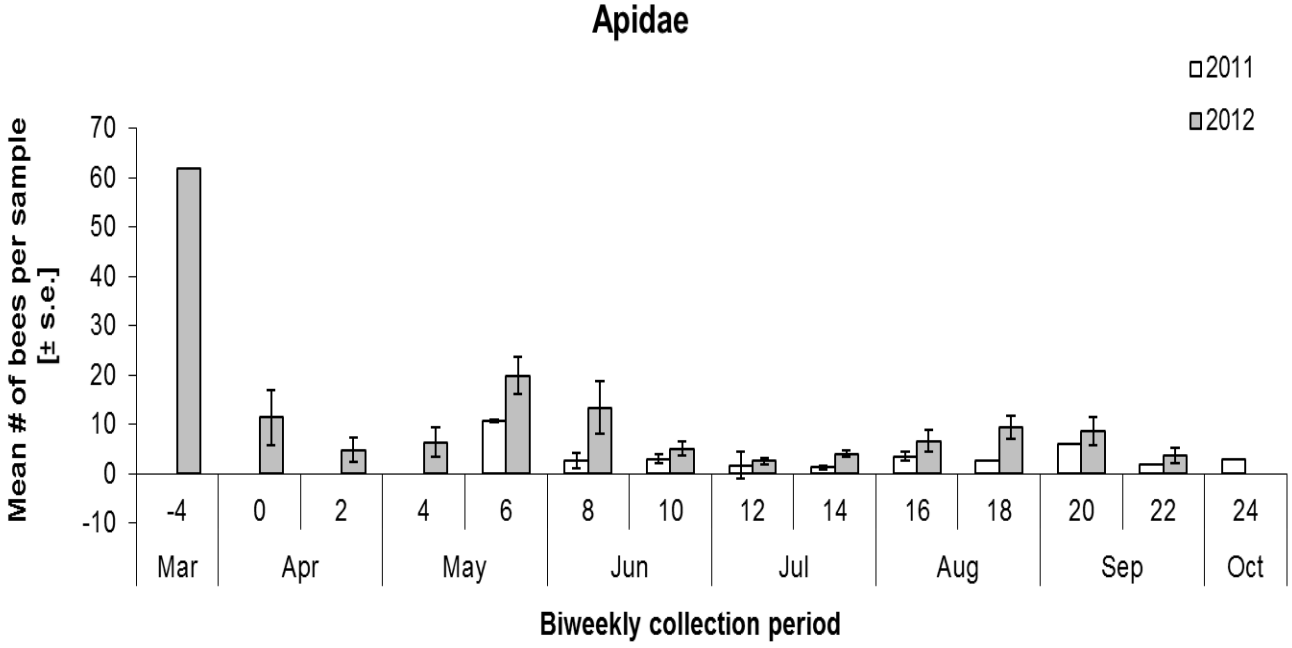
The five bee families Andrenidae, Apidae, Colletidae, Halictidae and Megachilidae were separately studied for phenology. The family Andrenidae in 2011 showed one peak of abundance in the spring (week 6), while it showed two peaks in 2012, the first in the early spring (week 0 and week 2) and the second in week 6 (Figure 3.2b). The family Apidae in 2011 showed two peaks of abundance, the first peak in the

a)

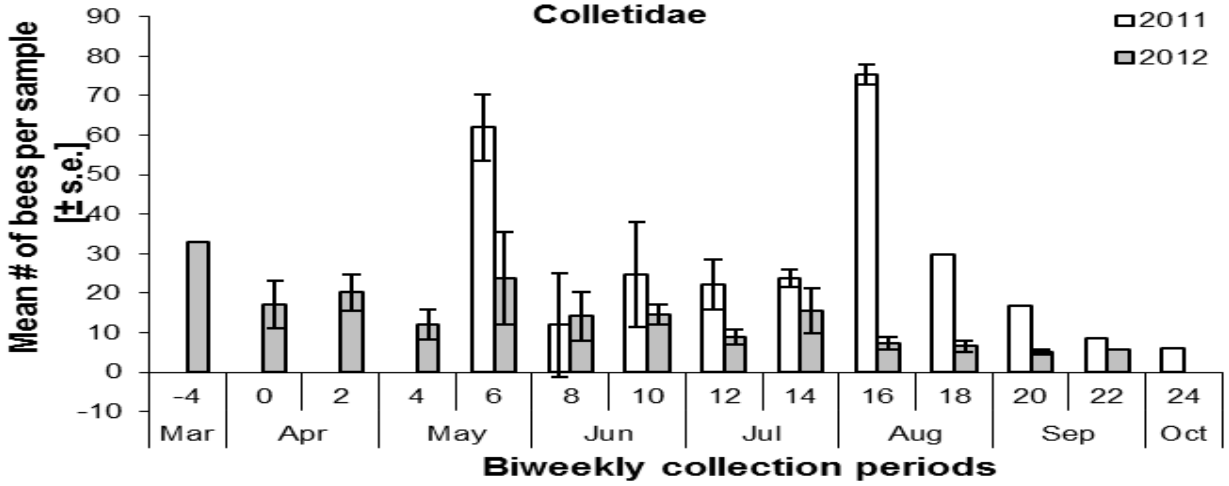

All Bees
2011
2012
Mean # of bees per sample [± s.e.]
180
160
140
120
100
80
60
40
20
0
-4
0
2
4
6
8
10
12
14
16
18
20
22
24
Mar
Apr
May
Jun
Jul
Aug
Sep
Oct
Biweekly colletion periods

b)

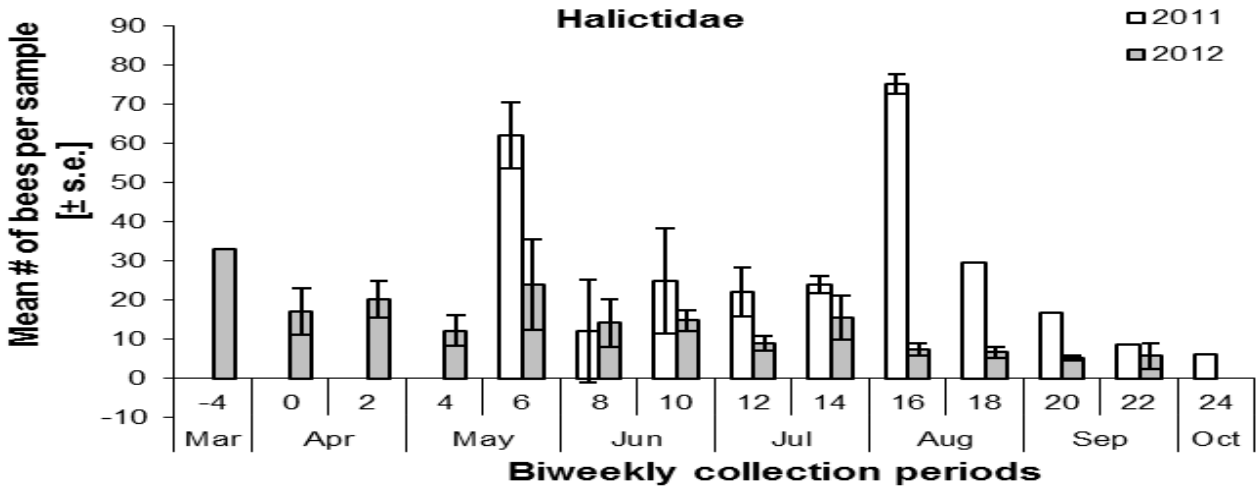

Andrenidae
Mean # of bees per sample [± s.e.]
3.5
3
2.5
2
1.5
1
0.5
0
2011
2012
-4
0
2
4
6
8
10
12
14
16
18
20
22
24
Mar
Apr
May
Jun
Jul
Aug
Sep
Oct
Biweekly collection periods


Apidae
2011
2012
Mean # of bees per sample [± s.e.]
70
60
50
40
30
20
10
0
-10
-4
0
2
4
6
8
10
12
14
16
18
20
22
24
Mar
Apr
May
Jun
Jul
Aug
Sep
Oct
Biweekly collection period

d)



e)



f)

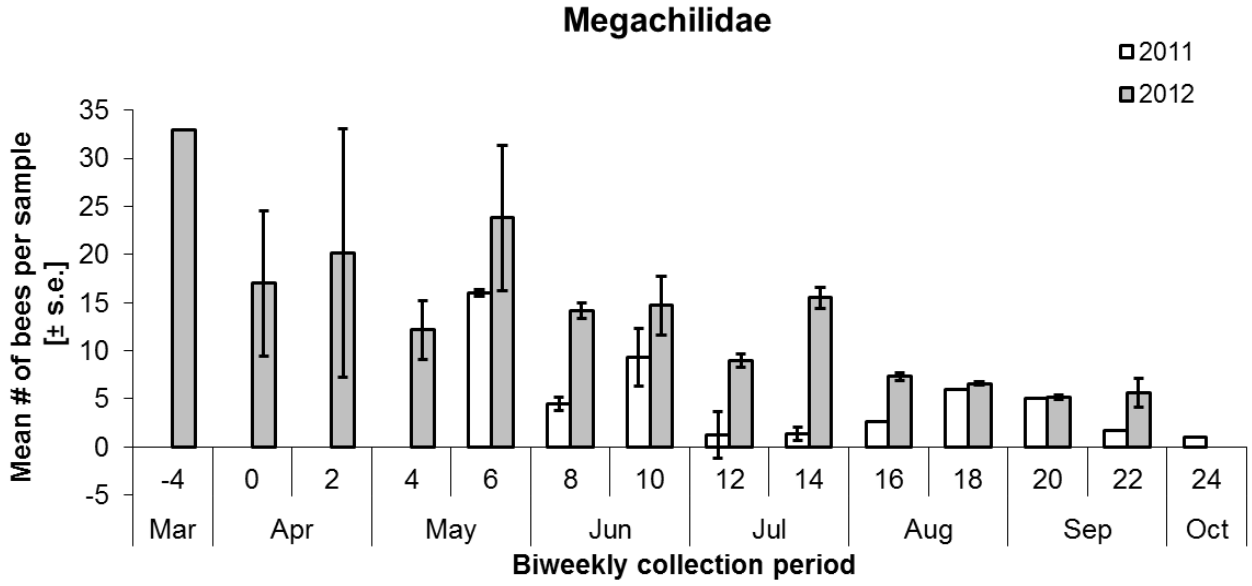


Figure 3.2. Biweekly mean number of bees per sample of all bees collected in pan traps and for each family from all restoration level sites combined from control site Brock south, old restoration sites Pond and Escarpment at Glenridge Quarry Naturalization site, and new restoration sites Elm1, Elm2 at Elm Street Naturalization site at Port Colborne, and station site at Wainfleet, Ontario for 2011 and 2012.

spring (week 6-8), and late summer (week 18-20) (Figure 3.2c). The most abundant apid species was *Ceratina mikmaqi* representing 23% of all Apidae. The family Colletidae had two peaks of abundance in 2011, during weeks 6 and 16, while in 2012 it had two peaks of abundance, weeks - 4 and 6 (Figure 3.2d). The most abundant species was *Hylaeus affinis* with 30% of all Colletidae members. The family Halictidae in 2011 showed two peaks in weeks 6 and 16, while in 2012 its peaks were at weeks - 4 and 6 (Figure 3.2e). The most abundant bee species was *Augochlorella aurata* with 34% of all Halictidae. The family Megachilidae in 2011 had two peaks in weeks - 4 and 6, while in 2012 it showed three peaks in weeks - 4, 6, and 14 (Figure 3.2f). *Osmia conjuncta* was the most abundant with 63% of all Megachilidae members.

3.3. Abundance of the bee community

3.3.1. Family abundance and patterns in different levels of restoration

The results show that the explanatory variables biweekly collection period, family, year, species, and site had a significant impact on bee abundance, while the restoration level did not have a significant impact (GLM test, Table 3.2, Model 1) on Log abundance of overall bees. In 2011, the difference in bee abundance among biweekly collection periods was caused by the week 6 and 16 collection periods, which had higher abundance than other periods, and week the 22 and 24 collection period, which had the lowest bee abundance. In 2012, the difference was caused by the week -4 and 6 period which had higher abundance than other periods, and the week 22 period, which had the lowest bee abundance (Figure 3.3). Different numbers of bees were caught during sampling collection periods. In both years, Halictidae was the most abundant family,

Table 3.2. The main and partial effects of general linear model on the total abundance of all bee families and for each family separately. Statistically significant effects in **bold**. n.s. means effects not statistically significant.

Model Number	Model	Effects	*d.f.*	*F*	*p*	R^2
1	**Log abundance of Overall (** number of bees per Morphospecies per Site per Biweekly Collection period per Year), of 2011-2012 ~ BiweeklyColl+ Family+ Year+ RestLevel+ Family/Species+ RestLevel/Site	Overall	103 and 813	3.302	**<2.2e-16**	0.2056
		Biweekly Collection periods	18	3.105	**1.488e-05**	
		Family	3	2.610	**0.050**	
		Year	1	4.013	**0.045**	
		Restoration level	2	0.926	n.s.	
		Species within Family	77	3.434	**<2.2e-16**	
		Site within Restoration level	2	3.011	**0.050**	
2	**Log abundance of Halictidae (** number of Halictidae bees per Morphospecies per Site per Biweekly Collection period per Year), of 2011-2012 ~ BiweeklyColl+ Species+ Year+ RestLevel+ RestLevel/Site	Overall	55 and 445	4.038	**<2.2e-16**	0.2505
		Biweekly Collection periods	15	2.022	**0.013**	
		Species	35	4.888	**3.525e-16**	
		Year	1	13.792	**0.0002**	
		Restoration level	2	0.979	n.s.	
		Site within Restoration level	2	2.451	**0.087**	
3	**Log abundance of Colletidae (** number of Colletidae bees per Morphospecies per Site per Biweekly Collection period per Year), of 2011-2012 ~ BiweeklyColl+ Species+ Year+ RestLevel+ RestLevel/Site	Overall	22 and 53	1.798	**0.042**	0.1897
		Biweekly Collection periods	13	1.240	n.s.	
		Species	4	2.250	**0.076**	
		Year	1	0.462	n.s.	
		Restoration level	2	6.465	**0.003**	
		Site within Restoration level	2	0.524	n.s.	

Table 3.2. Continue

Model Number	Model	Effects	*d.f.*	*F*	*P*	R^2
4	**Log abundance of Megachilidae (** number of Megachilidae bees per Morphospecies per Site per Biweekly Collection period per Year), of 2011-2012 ~ BiweeklyColl+ Species+ Year+ RestLevel+ RestLevel/Site	Overall	40 and 95	2.688	**4.444e-05**	0.3334
		Biweekly Collection periods	16	2.788	**0.001**	
		Species	19	2.694	**0.0008**	
		Year	1	0.859	n.s.	
		Restoration level	2	3.753	**0.027**	
		Site within Restoration level	2	1.681	n.s.	
5	**Log abundance of Apidae (** number of Apidae bees per Morphospecies per Site per Biweekly Collection period per Year), of 2011-2012 ~ BiweeklyColl+ Species+ Year+ RestLevel+ RestLevel/Site	Overall	39 and 164	2.911	**1.256e-06**	0.2685
		Biweekly Collection periods	15	4.391	**6.785e-07**	
		Species	19	2.107	**0.006**	
		Year	1	3.754	**0.054**	
		Restoration level	2	0.828	n.s.	
		Site within Restoration level	2	1.109	n.s.	

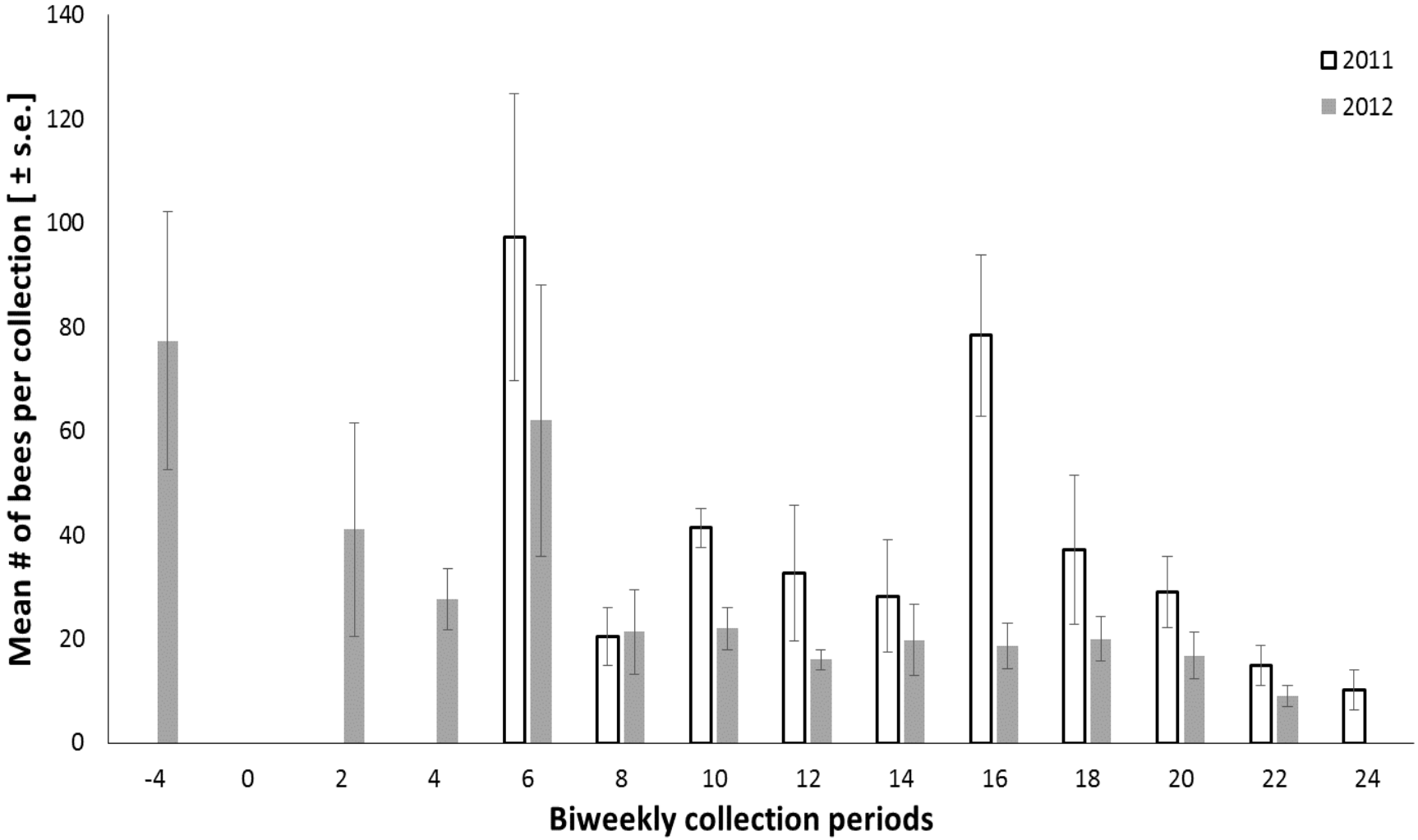


Figure 3.3. The distribution of the mean number of bees per collection of 2011-2012 among the biweekly collection periods. There were differences in bee abundance among the biweekly collection periods.

while Colletidae was the least abundant (Figure 3.4). There were more bees in 2012 than 2011 in all families, except Halictidae (Figure 3.4). There were massive declines in bee abundance in 2012 (Figure 3.5). There was a significant difference in the bee abundance among species. *L. (Dialictus) hitchensi* was the most abundant species. There were also different numbers of bees caught in different sites. BrS and Esc sites had more bees in 2012 than 2011, while Pon, Em2 and StR had fewer bees in 2012 than 2011 (Figure 3.6). The biggest decline was at StR site where the number of bees declined from 511 bees in 2011 to 222 bees in 2012. That decline was caused by the subgenus *L. (Dialictus)*, which are mostly underground nesters that were badly affected by the drought in 2012 (Table 3.3). There were no significant differences in bee abundance among restoration levels which means different restoration levels had the same numbers of bees (Figure 3.7.). In other words, restoration positively increased the abundance of bees in the newly restored sites and the result was difference in bee abundance between control and newly restored sites.

Halictidae abundance in 2011 and 2012

The general linear model results showed biweekly collection periods, species, year and site had a significant impact on Halictidae abundance, while restoration level did not have significant impact (GLM test, Table 3.2, Model 2). Different numbers of halictid bees were caught during the sampling collection periods. In 2011, the difference was caused by the biweekly collection periods 6 and 16, which had higher abundance than

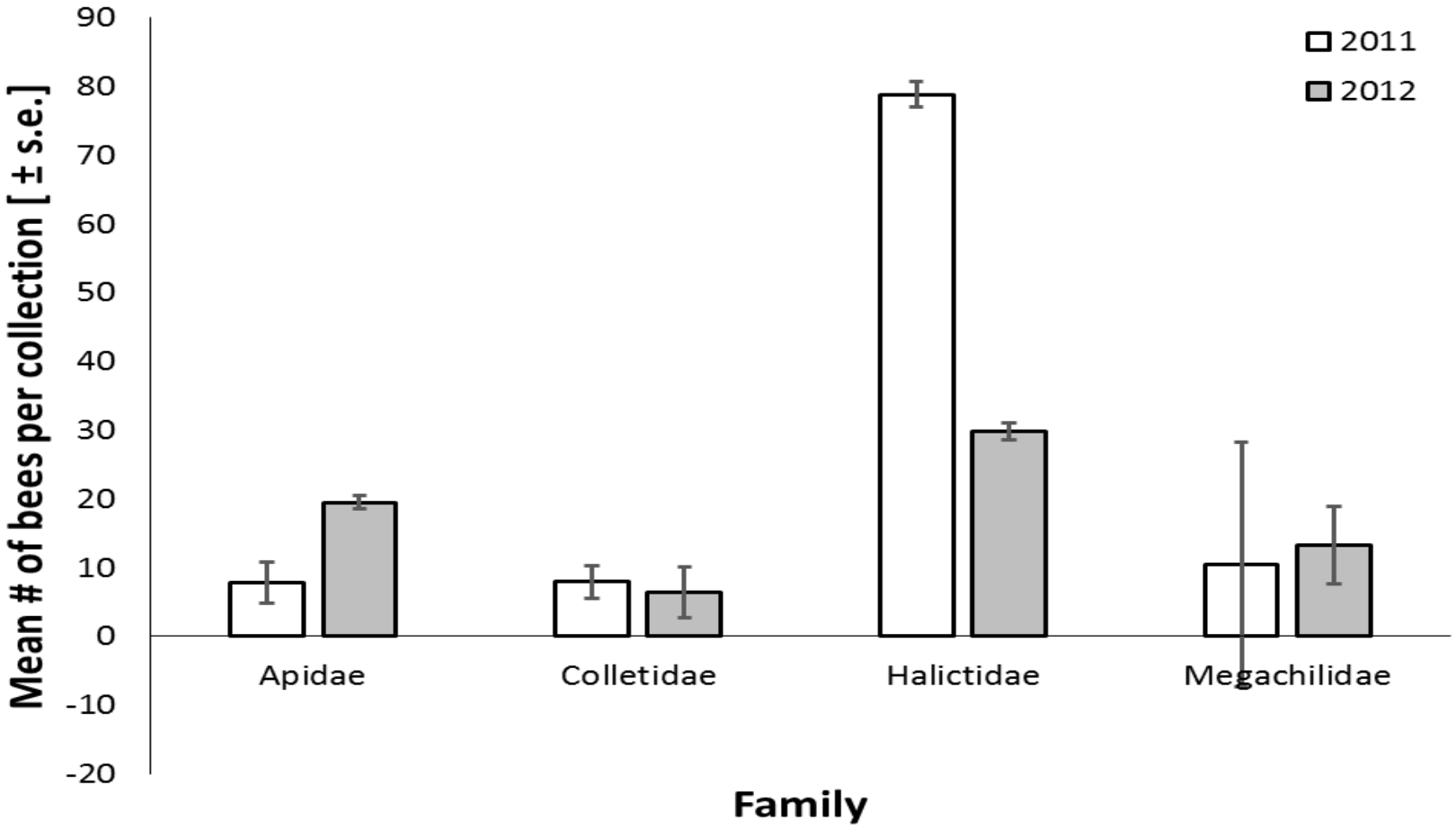


Figure 3.4. The distribution of the mean number of bees per collection among bee families of 2011 and 2012. There was a difference in bee abundance among families.

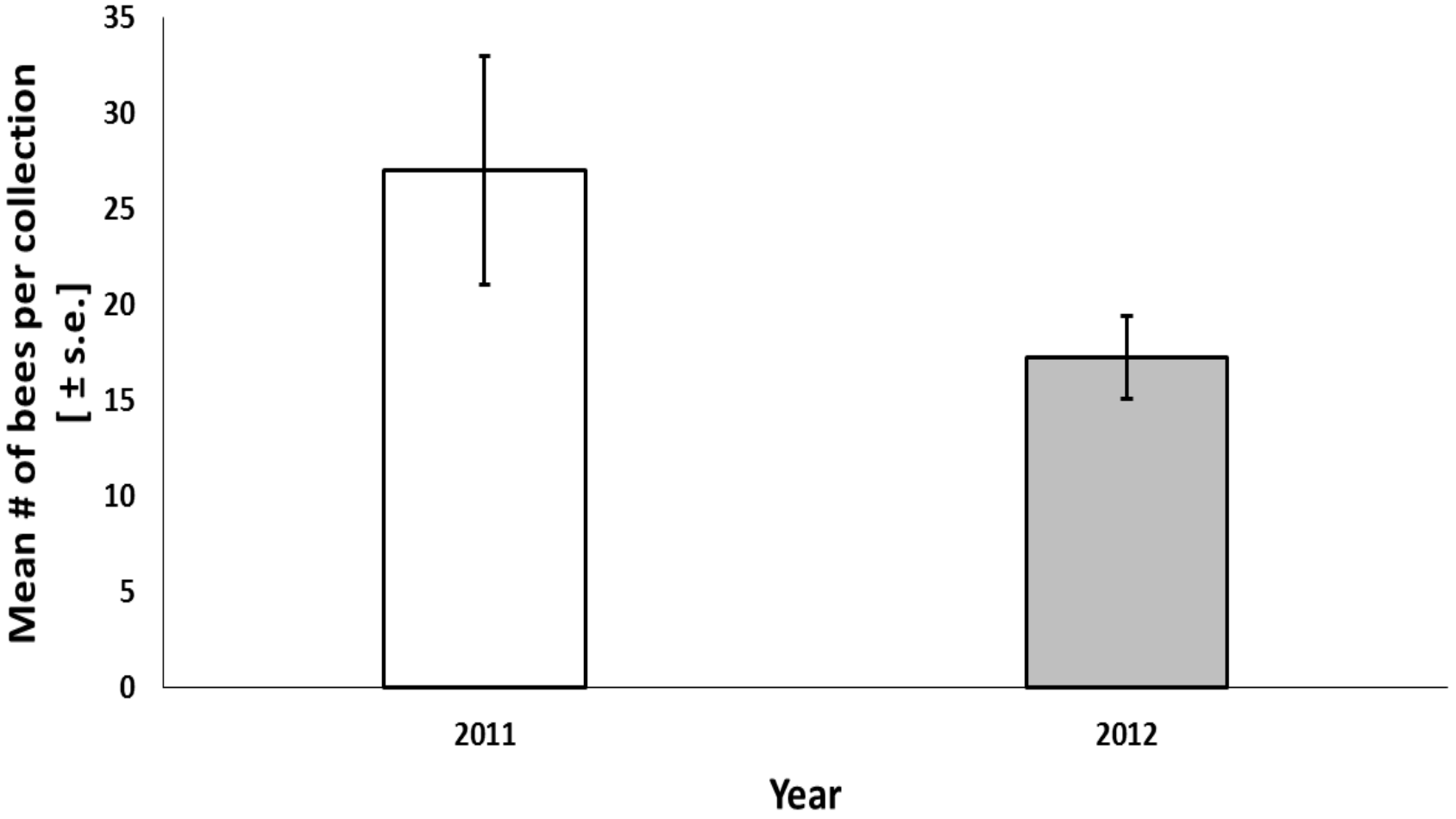


Figure 3.5. The distribution of the mean number of bees per collection between years. There were differences in bee abundance among bees. In 2011 more bees were caught than 2012.

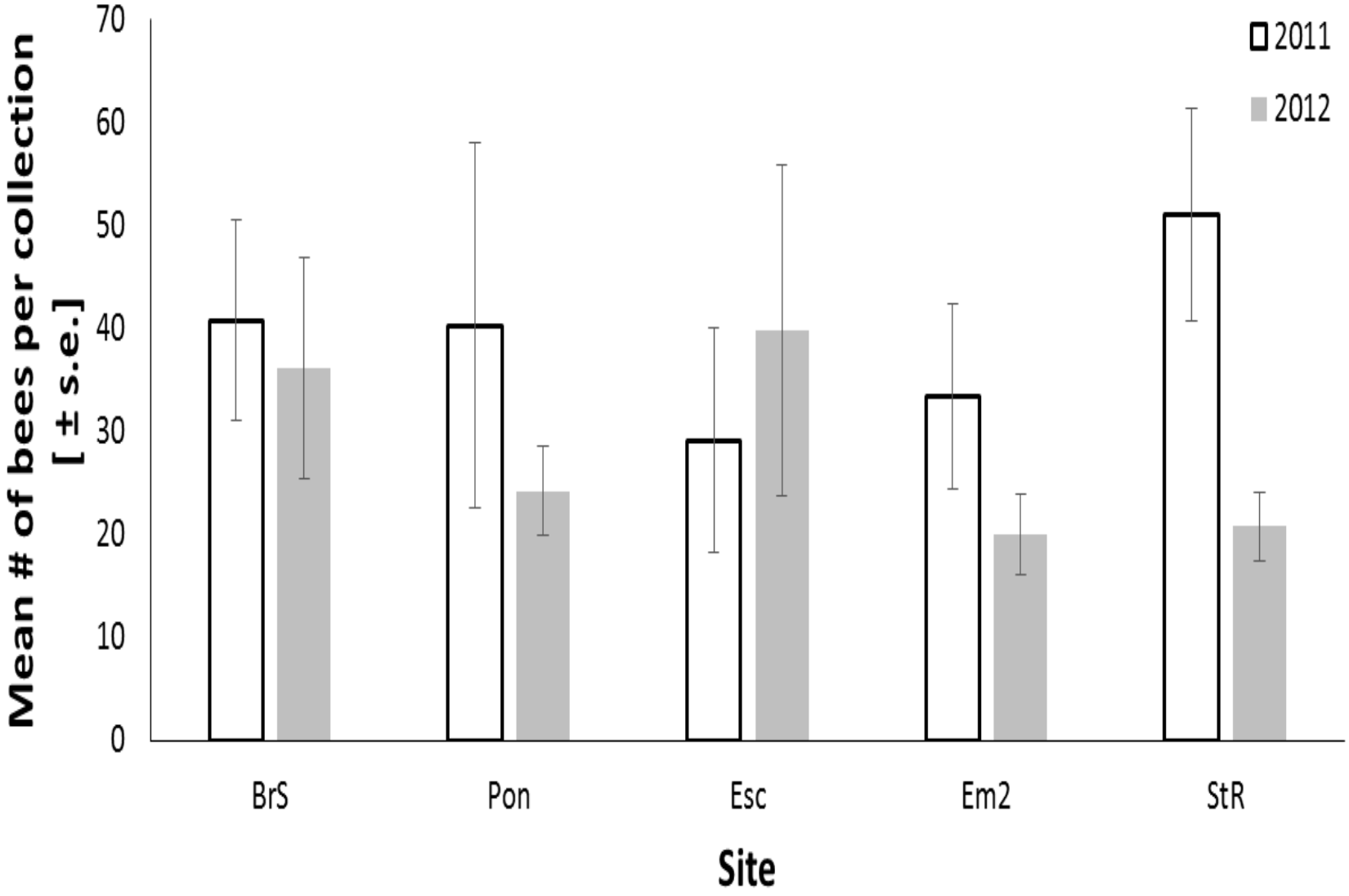


Figure 3.6. The distribution of the mean number of bees per collection among sites of 2011 and 2012. There were a differences in bee abundance among sites. Pon, Em2, and StR had a lower number of bees in 2012 than 2011.

Table 3.3. Difference in bee genera mean abundance of Station Road (StR) 2011 and 2012

Family	**Genus**	**Mean number of bees per collection period**	
		2011	2012
Apidae	*Anthophora*	1	1
	Apis	1	1.4
	Bombus	1	1.2
	Ceratina	1	2.5
	Melissodes		2
Colletidae	*Hylaeus*	1.2	4
Halictidae	*Augochlora*		2
	Augochlorella	1.8	1.7
	Halictus	2.9	3.7
	L. (Dialictus)	19.3	12.2
	Lasioglossum	7.3	2.17
Megachilidae	*Anthidium*	1	1
	Coelioxys	1	1
	Hoplitis	1	
	Megachile	1	1.8
	Osmia	2	1
	Stelis		1

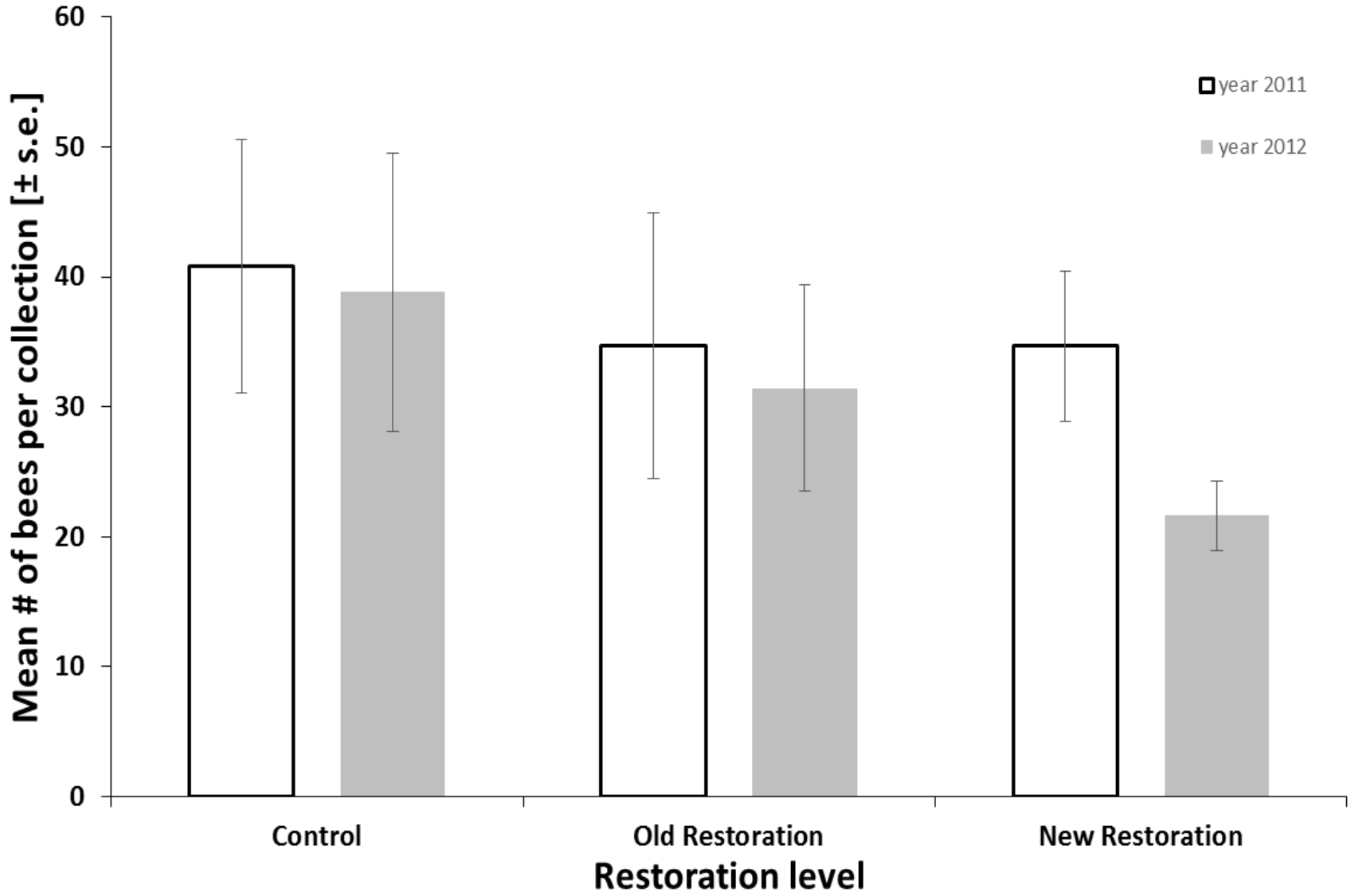


Figure 3.7. The distribution of the mean number of bees per collection among restoration levels of 2011 and 2012. There were no differences in bee abundance among restoration levels.

other periods, and week 24 period which had the lowest bee abundance. In 2012, the difference was caused by the biweekly collection periods -4 and 6, which had the highest abundance, while the biweekly collection period 22 had the lowest abundance (Figure 3.8). There was a significant difference in halictid abundance among species (Table 3.4). There were different numbers of bees caught during the sample years: 2011 had more bees than 2012 (Figure 3.9). There were no significant differences in Halictidae abundance between restoration levels, which means different restoration levels had the same number of bees (Figure 3.10). There were significant differences in number of bees caught in the different sites but there was a major decline in halictidae (Figure 3.11).

Colletidae abundance in 2011 and 2012

The general linear model result (GLM test, Table 3.2, Model 3) showed that biweekly collection period, year, restoration level, and sites nested under restoration levels had no impact on Colletidae abundance. In 2011 and 2012 there was the same Colletidae abundance among the biweekly collection periods (Figure 3.12). There were no significant differences in Colletidae among the biweekly collection periods (Table 3.2, Model 3). There was no difference in Colletidae bees caught in 2011and 2012 (Figure 3.13). There were no differences in number of Colletidae bees caught in different sites (Figure 3.14). The Colletidae abundance of 2011 and 2012 was significantly different among species (Table 3.5). There was a significant difference in Colletidae abundance among restoration levels, which means that different restoration levels had different numbers of bees. In 2011, the control level had more colletid bees than other levels, while in 2012 the three restoration levels had the same number of Colletidae bees(Figure 3.15).

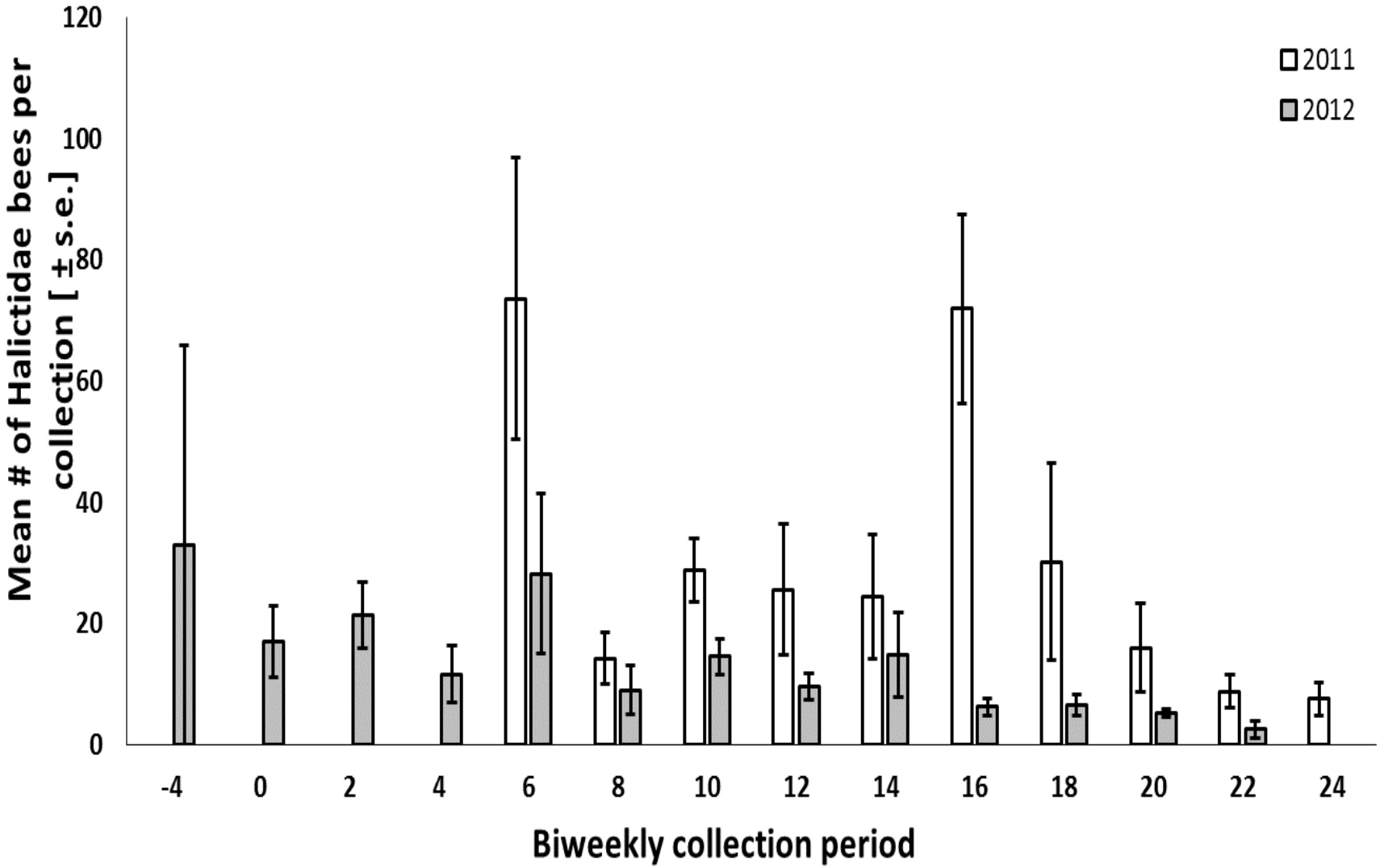


Figure 3.8. The distribution of the mean number of Halictidae bees per collection among biweekly collection periods. There were significant differences in Halictidae abundance among biweekly collection periods.

Table 3.4. Mean number of Halictidae bees per collection period in all sites. The most abundant species was *L. (Dialictus) hitchensi*, which had sharp decline in 2012.

Family	Genus	Species	Mean number of bees per collection period	
			2011	2012
Halictidae	*Agapostemon*	*virescens*	1.7	1.6
	Augochlora	*pura*	1.4	2
	Augochlorella	*aurata*	26.3	13.6
	Halictus	*confusus*	2.5	3.1
		ligatus	4.2	2.8
		rubicundus	1	1
	L. (Dialictus)	*admirandum*	8.5	6.1
		atwoodi	1.3	2
		cressonii	1	1.5
		ellisiae		1
		ephialtum	1.7	1
		fattigi	1	1
		hitchensi	26.7	6.9
		imitatum	2.7	1
		laevissimum	1.7	1.2
		leucocomum	1	
		lineatulum	1	
		nigroviride		1
		nymphaearum	1	1.5
		oblongum	1.5	2
		paradmirandum	6.5	2.2
		perpunctatum	2	
		pilosum	15.4	3.1
		sagax	1	
		versatum	10.1	1.7
		viridatum	1.2	1
		weemsi	1.3	
		zephyrum	1	1
	L. (Evylaeus)	*cinctipes*		1
	Lasioglossum	*coriaceum*	2	2.2
		leucozonium	2.4	2
		zonulum	5.6	1.7
	Sphecodes	*atlantis*		1
		dichrous		1

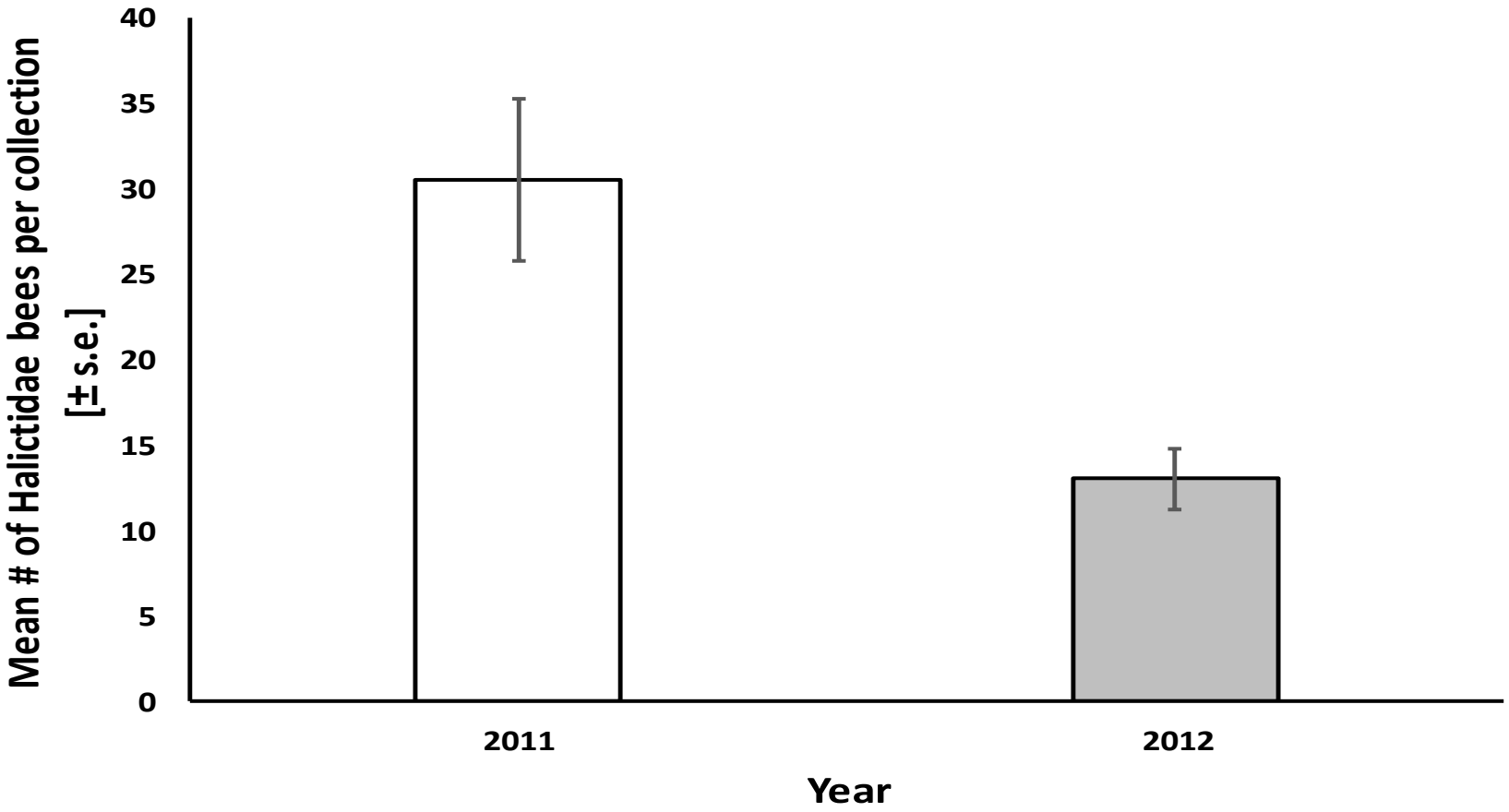


Figure 3.9. The distribution of the mean number of Halictidae bees per collection between years. There were significant differences in Halictidae abundance between years. The Halictidae abundance was higher in 2011 than in 2012.

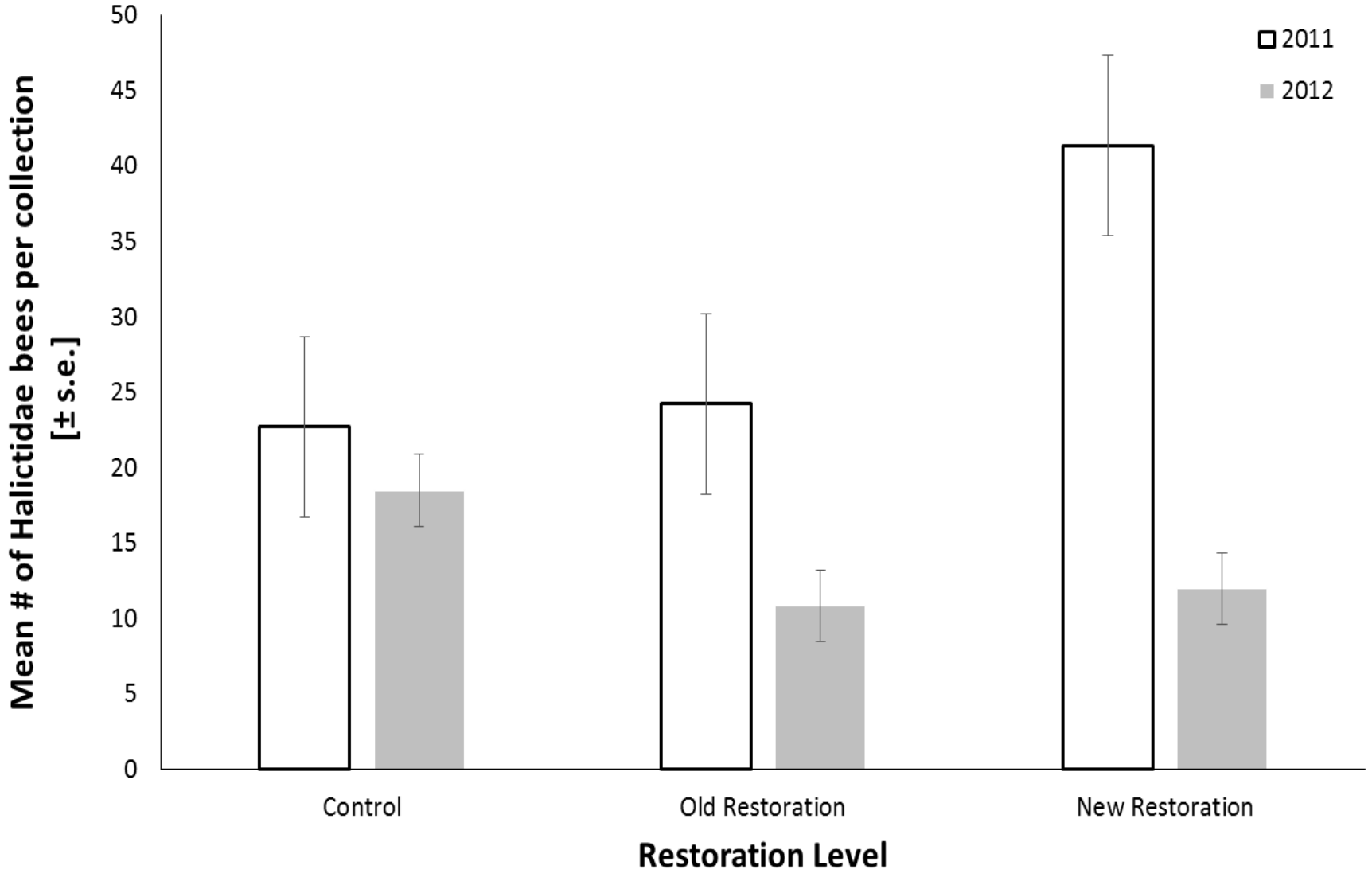


Figure 3.10. The distribution of the mean number of Halictidae bees per collection among the restoration levels for 2011 and 2012. There were no differences in Halictidae abundance among restoration levels.

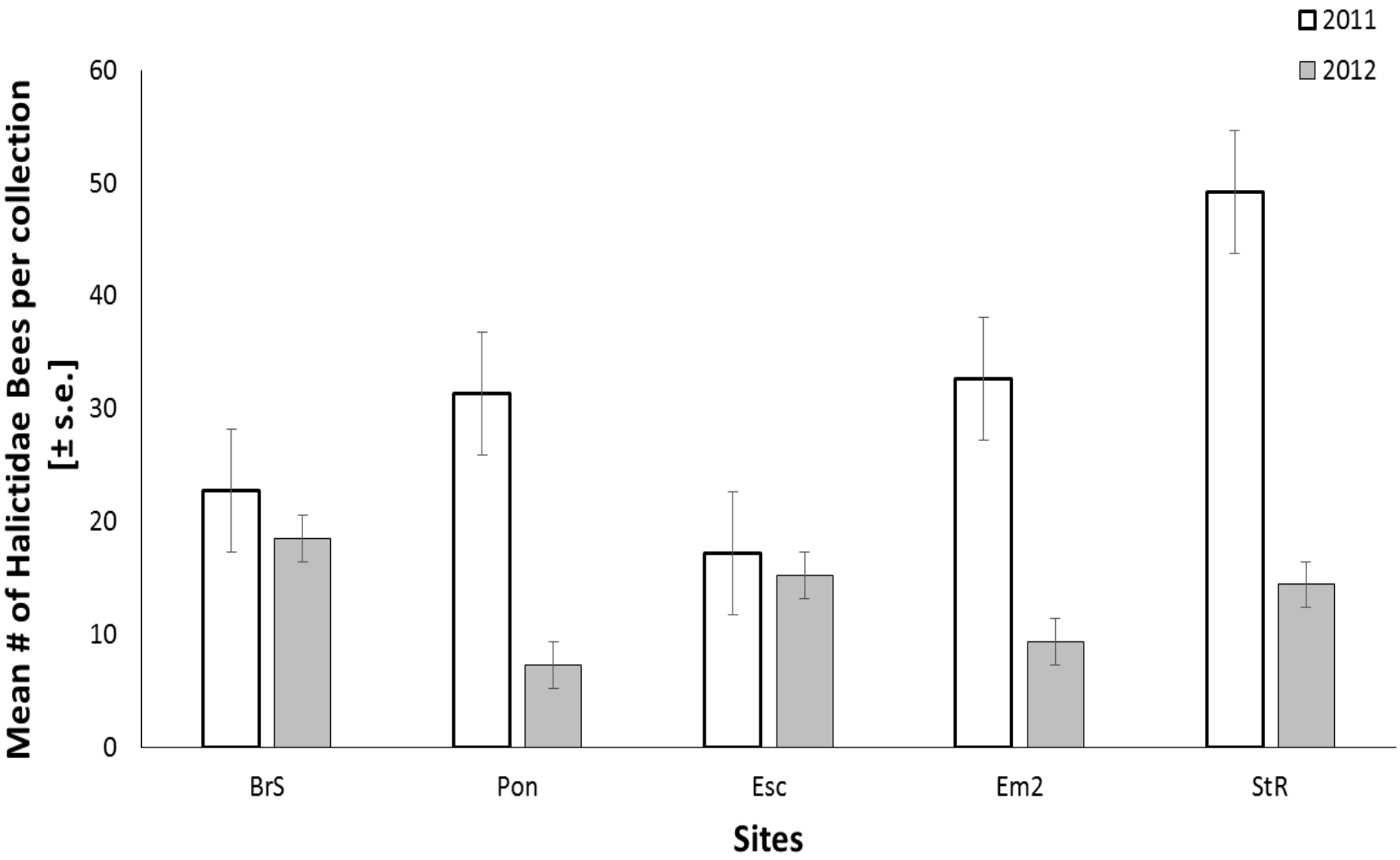


Figure 3.11. The distribution of the mean number of Halictidae bees per collection among sites of 2011 and 2012. There were significant differences in Halictidae abundance among sites. In 2011 StR had more bees than other sites while in 2012 Pon had a lower number of bees than other sites.

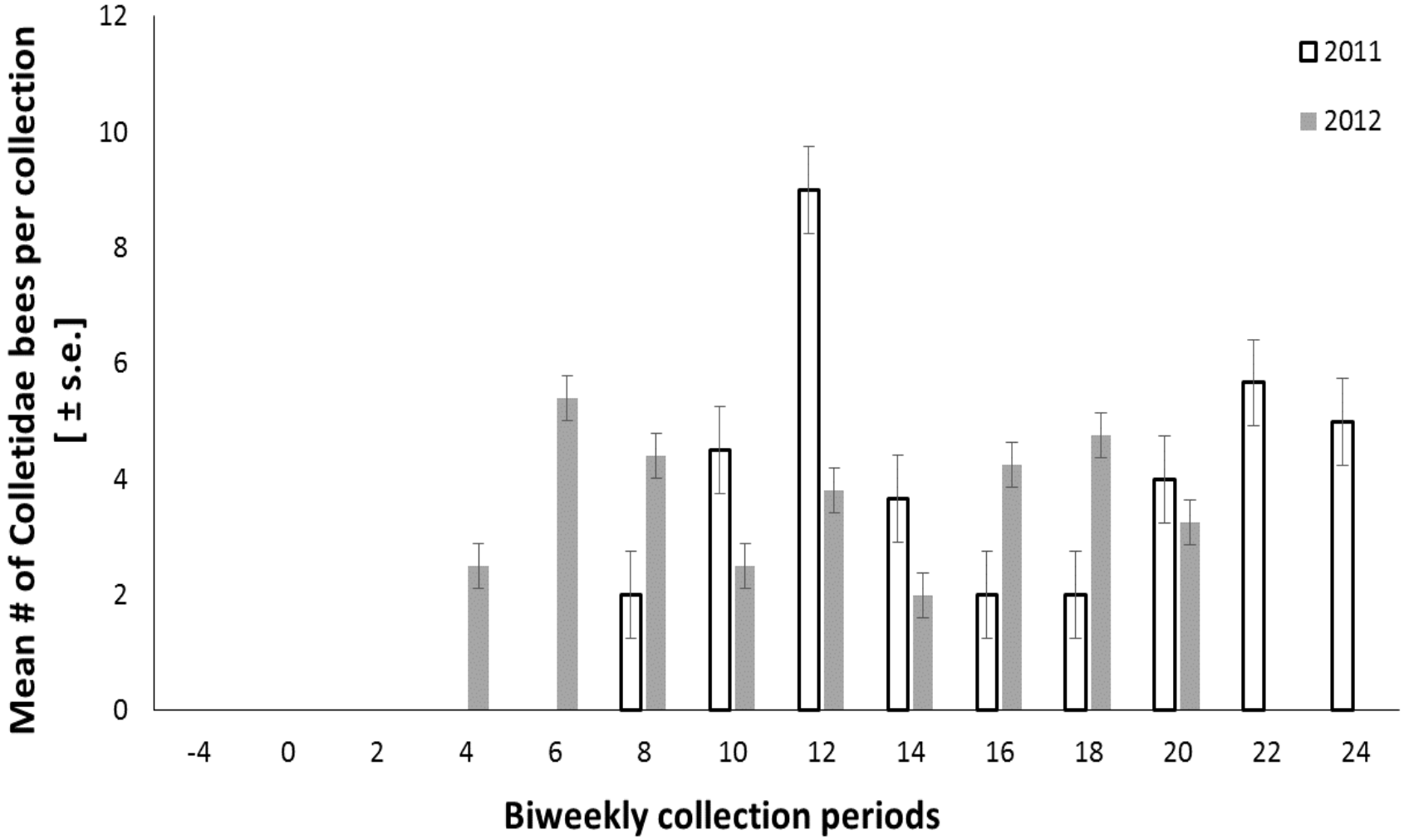


Figure 3.12. The distribution of the mean number of Colletidae bees per collection among biweekly collection periods of 2011 and 2012. There was no significant difference in Colletidae abundance among biweekly collection periods.

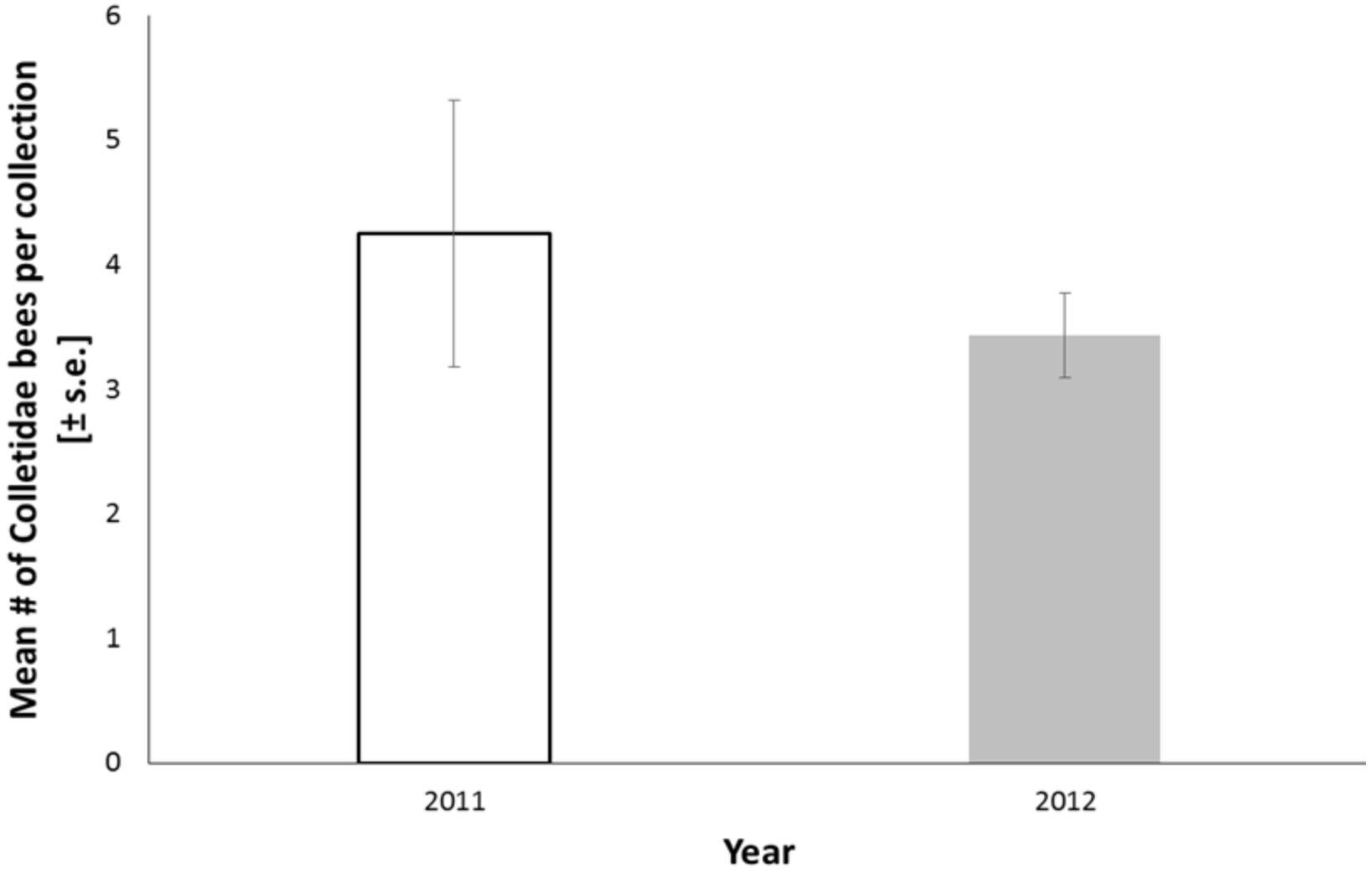


Figure 3.13. The distribution of the mean number of Colletidae bees per collection between years. There was no difference in Colletidae abundance between years.

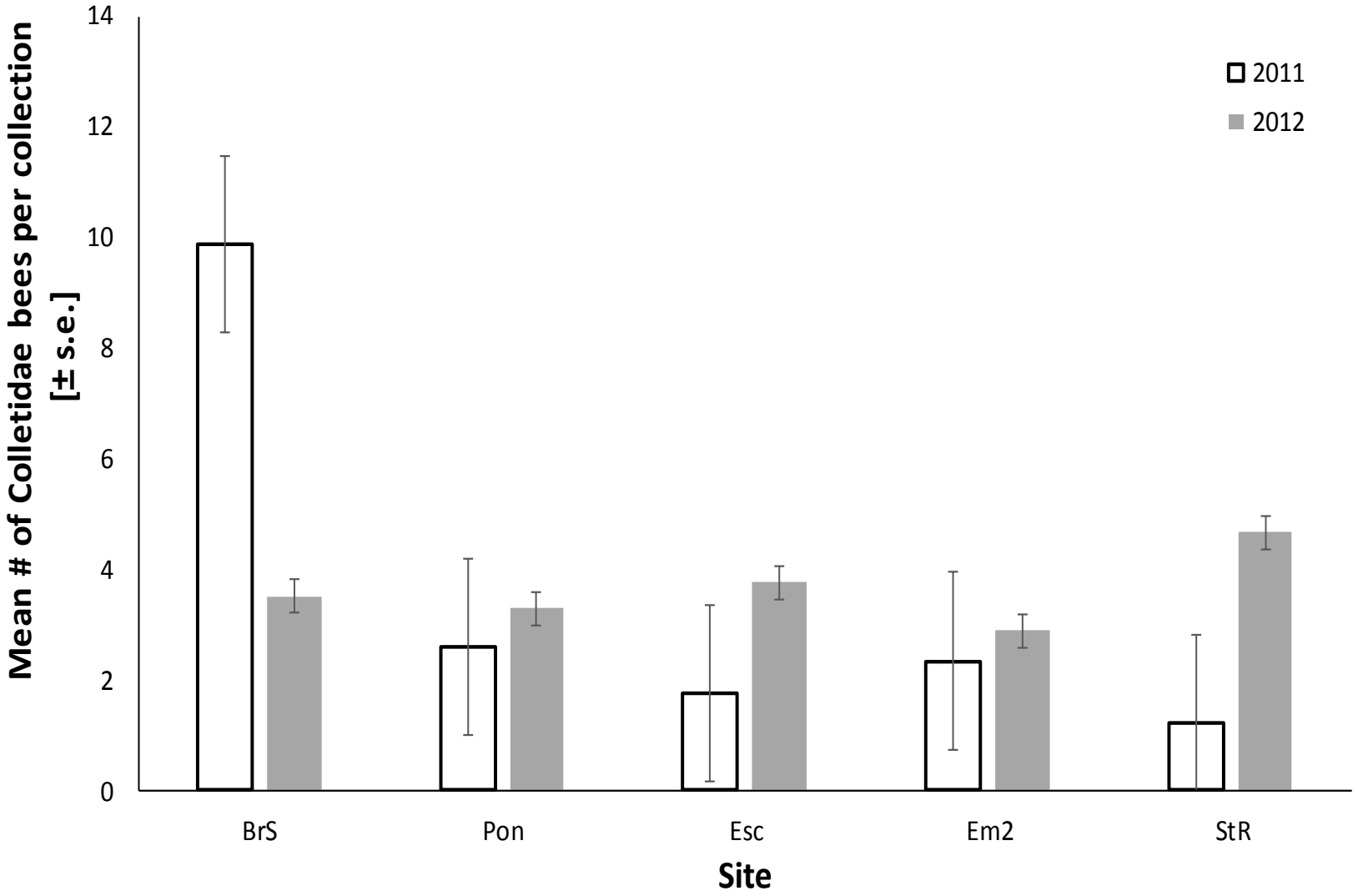


Figure 3.14. The distribution of the mean number of Colletidae bees per collection among sites of 2011 and 2012. There was no difference in Colletidae abundance among sites.

Table 3.5. Mean number of Colletidae bees per collection periods among species of all sites. There were differences in Colletidae abundance among species.

Genus	Species	Mean number of bees per collection period	
		2011	**2012**
Hylaeus	*affinis*	5.5	5.6
	annulatus	1.3	
	hyalinatus		1.5
	mesillae		1
	modestus	3.9	1

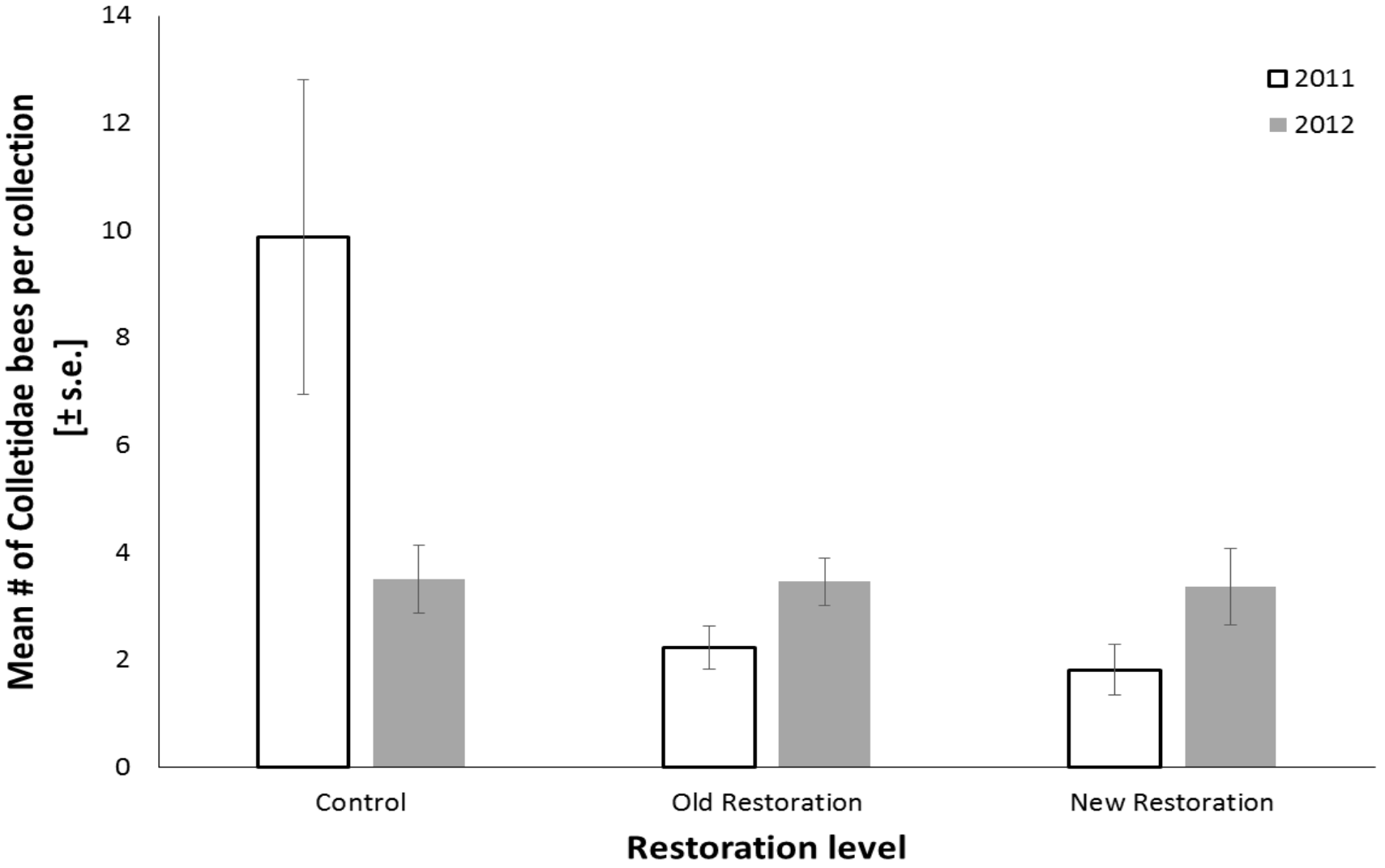


Figure 3.15. The distribution of the mean number of Colletidae bees per collection for restoration levels of 2011 and 2012. There was a significant difference in Colletidae abundance among restoration levels. In 2011, the control level had the highest Colletidae abundance.

Megachilidae abundance in 2011 and 2012

The general linear model results show that biweekly collection period, species, and restoration level had a significant impact on Megachilidae abundance, while year and site did not have significant impact (Table 3.2, Model 4). There were different numbers of Megachilidae bees caught during the biweekly collection periods. In 2011, the difference was caused by the biweekly collection period 6, which had higher Megachilidae abundance than other periods. In 2012, the biweekly collection period -4 had the highest Megachilidae abundance (Figure 3.16). There was a significant difference in Megachilidae abundance between species (Table 3.6). Also, there was a significant difference in Megachilidae abundance among restoration levels, meaning different restoration levels had different numbers of bees. The control and old restoration level had a higher number of bees than new restoration level (Figure 3.17). There were no differences in numbers of Megachilidae bees caught during 2011 and 2012 (Figure 3.18). There was no difference in abundance of Megachilidae bees caught in different sites (Figure 3.19).

Apidae abundance in 2011 and 2012

The general linear model results showed that biweekly collection period, species and year had a significant impact on Apidae abundance, while restoration level and site nested within restoration level did not have significant impact (Table 3.2, Model 5). There were different numbers of Apidae caught during the biweekly collection periods. In both years the difference was caused by biweekly collection period 6 which had higher Apidae abundance than other periods (Figure 3.20). There was a significant different in

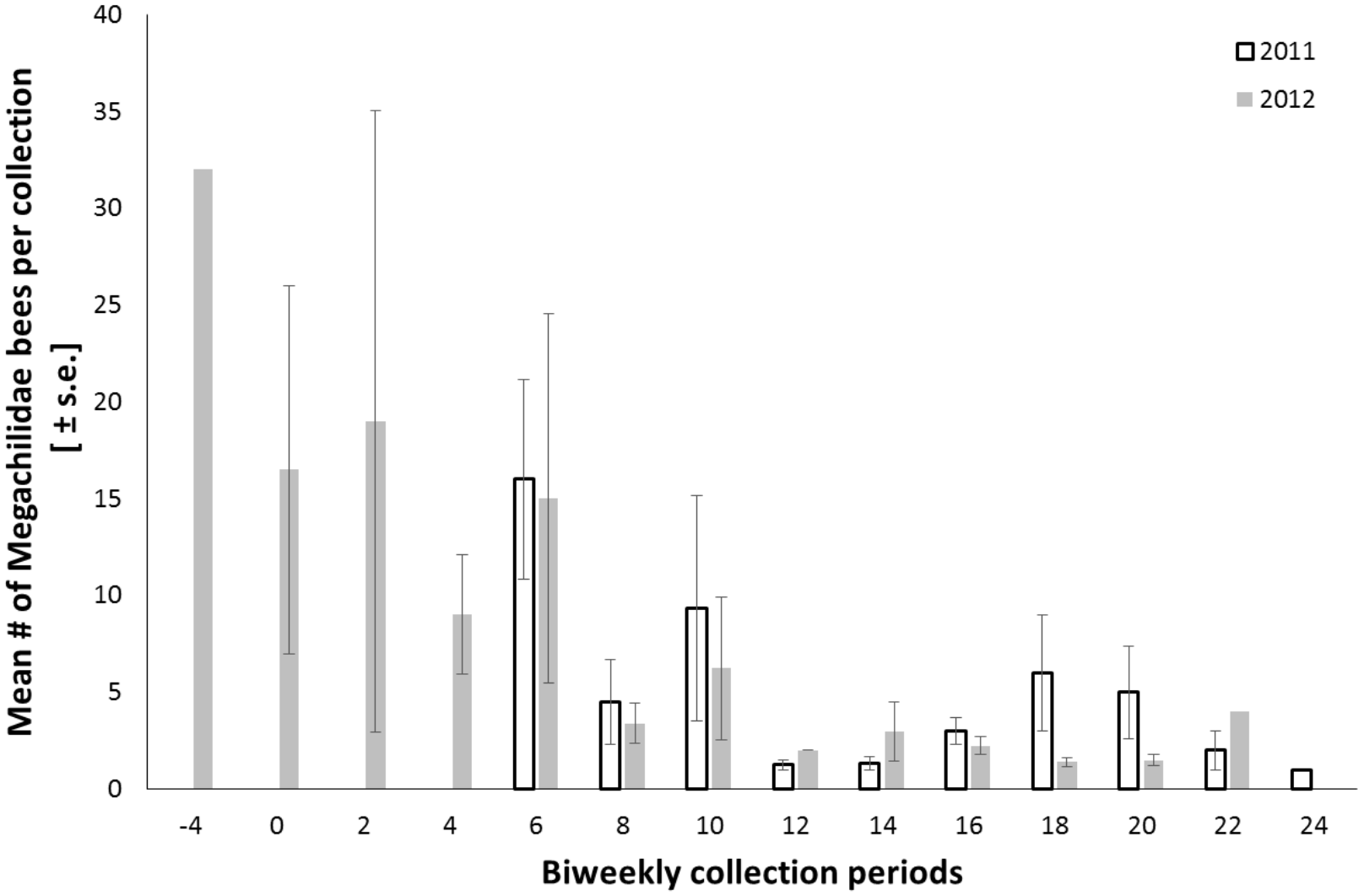


Figure 3.15. Colletidae abundance among restoration levels. There were significant differences in Colletidae abundance among restoration levels.

Table 3.6. Mean number of Megachilidae bees per collection periods among species of all sites. There were differences in Megachilidae abundance among species.

Genus	Species	Mean number of bees per collection period	
		2011	**2012**
Anthidium	*manicatum*	5.3	1
	oblongatum		1
Coelioxys	*octodentata*	1.5	1
	rufitarsis	2	1
Heriades	*carinatus*		1
	leavitti		1
	variolosa		1
Hoplitis	*pilosifrons*	1	1.7
	producta		1.5
	spoliata	1.5	2.7
Megachile	*brevis*	2.1	2.3
	campanulae		1
	ericetorum		1
	pugnata		1
	relativa	1	1
	rotundata	3	1
Osmia	*atriventris*	1	1.2
	conjuncta	14.1	20
	pumila	2	3.1
Stelis	*lateralis*	1	1

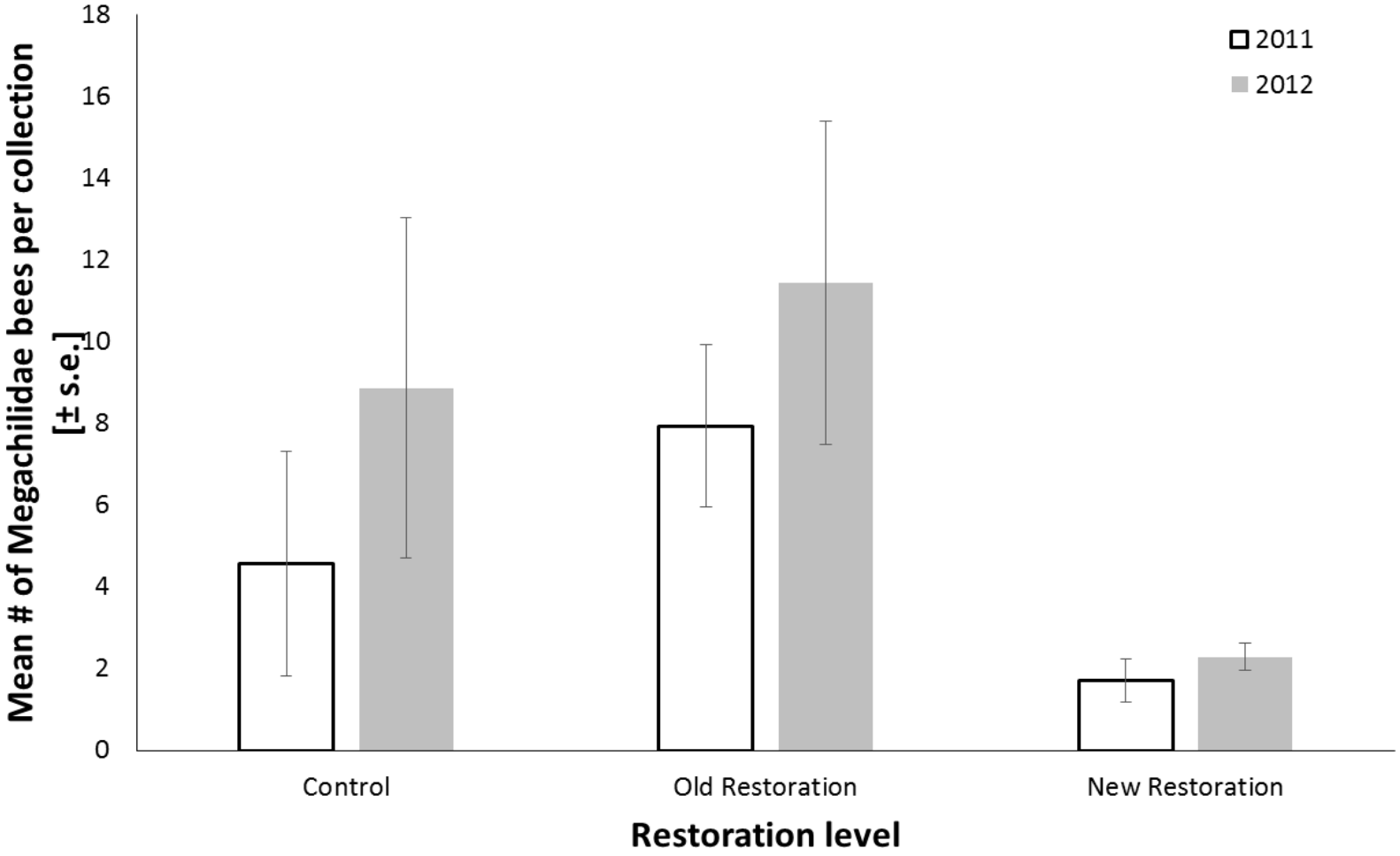


Figure 3.17. The distribution of the mean number of Megachilidae bees per collection among restoration levels for 2011 and 2012. There were significant differences in Megachilidae abundance between restoration levels.

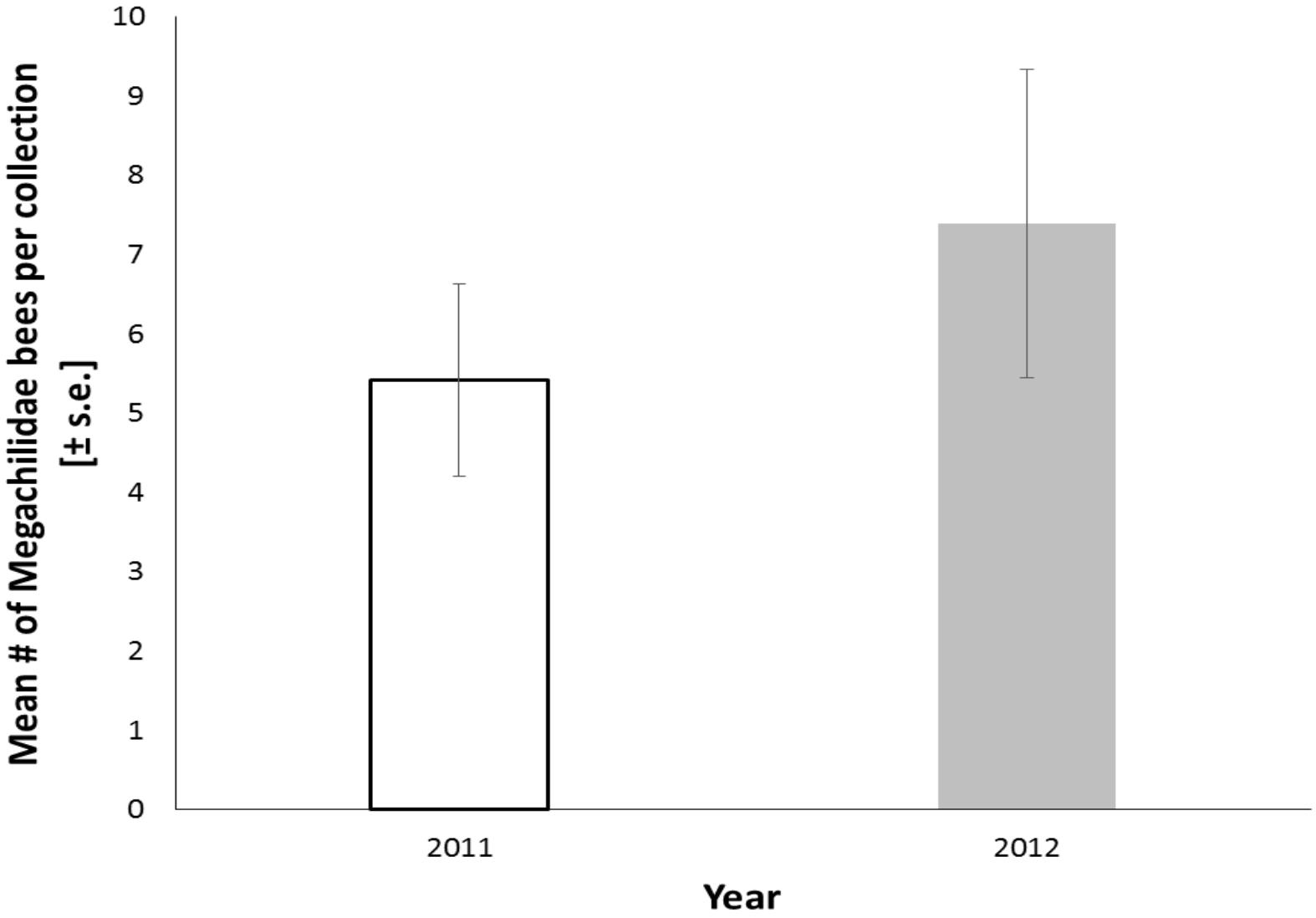


Figure 3.18. The distribution of the mean number of Megachilidae bees per collection between years 2012. There was no difference in Megachilidae abundance between years.

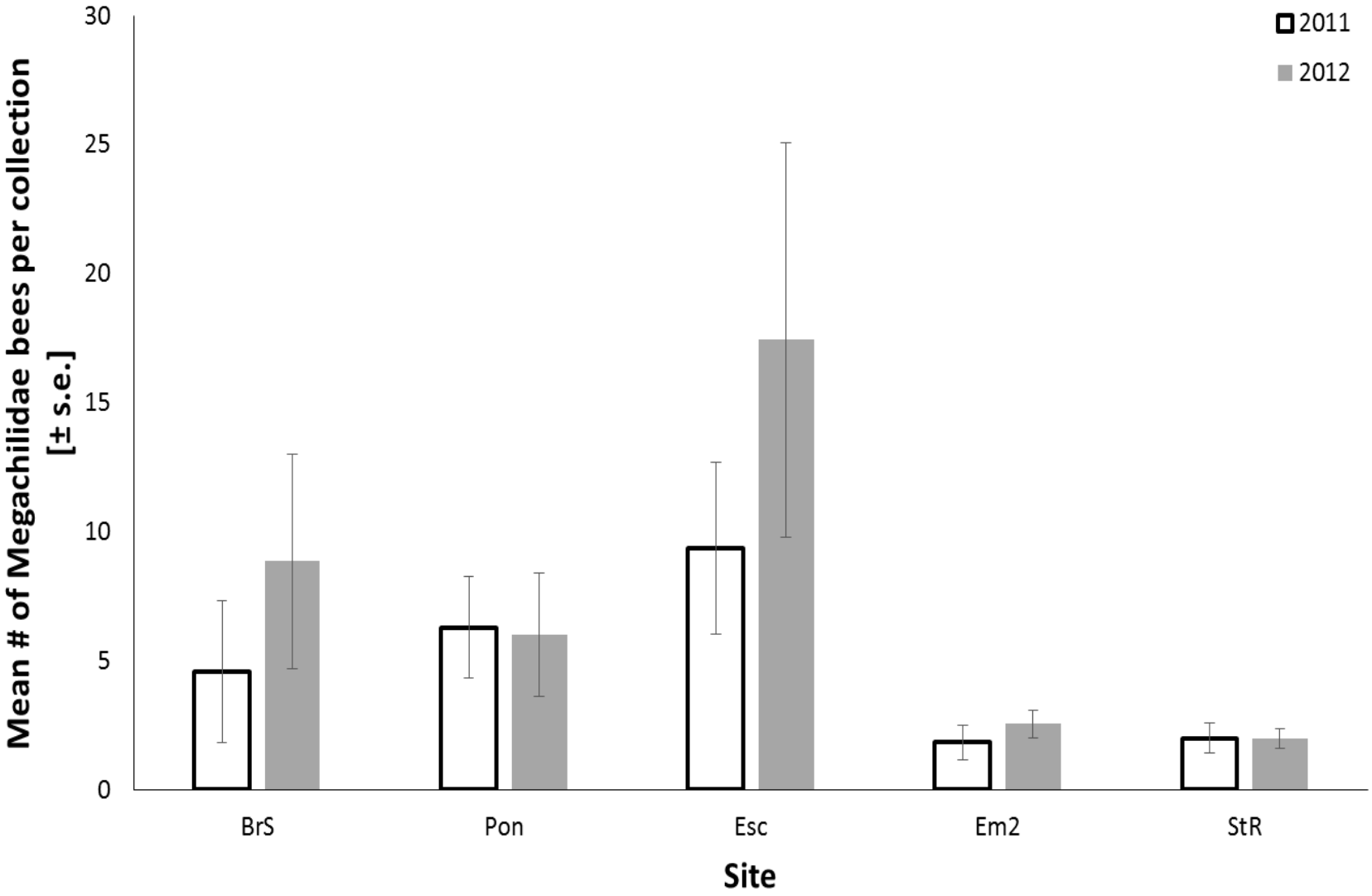


Figure 3.19. The distribution of the mean number of Megachilidae bees per collection among sites for 2011 and 2012. There was no difference in Megachilidae abundance among sites.

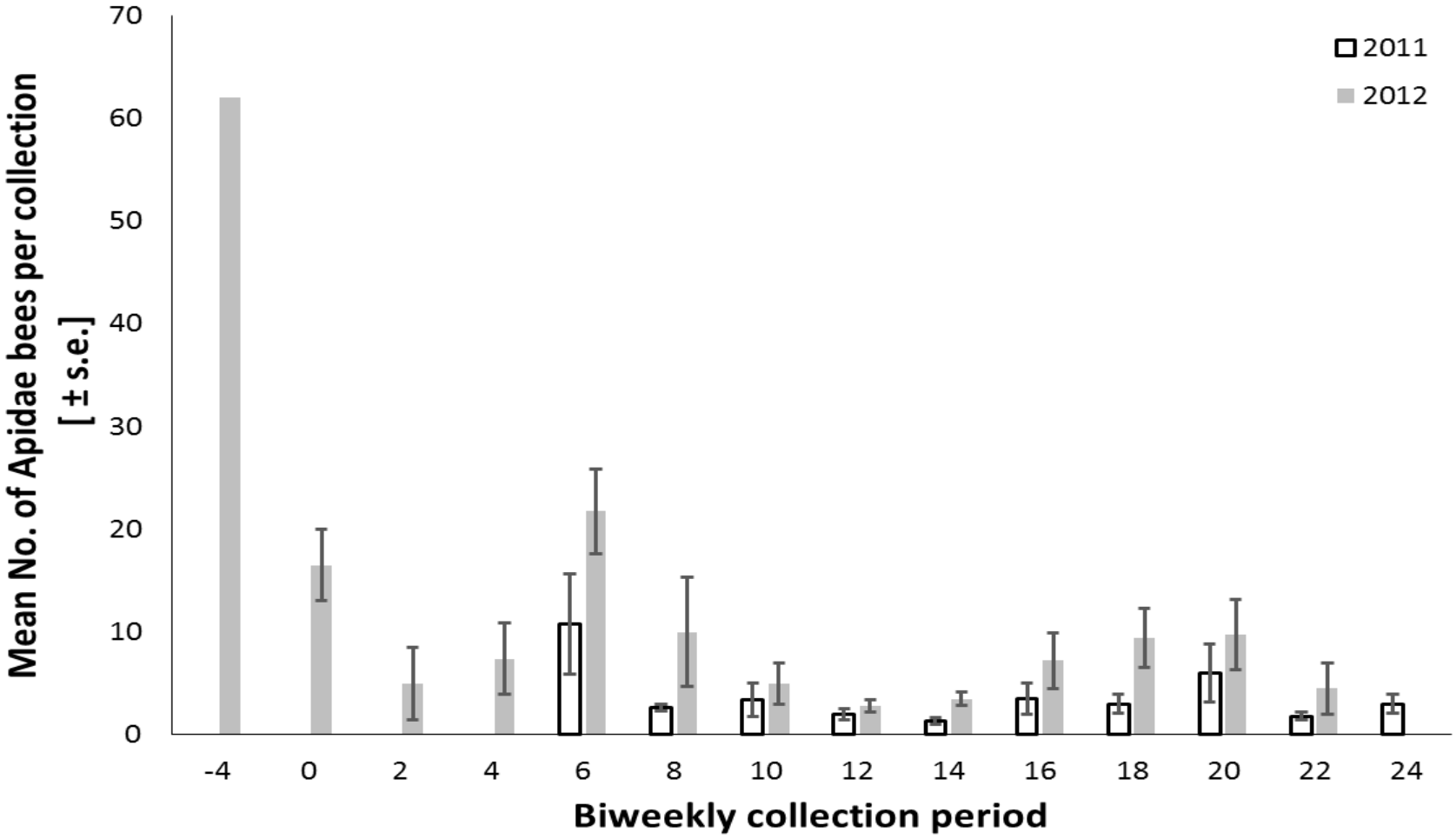


Figure 3.20. The distribution of the mean number of Apidae bees per collection among biweekly collection periods for 2011 and 2012. There were significant differences in mean abundance of Apidae among biweekly collection periods.

Apidae abundance among species (Table 3.7). In 2012 there were more Apidae bees than 2011. There were significant differences in Apidae abundance among years (Figure 3.21). There were no significant differences in Apidae abundance among restoration levels, so different restoration levels had the same number of Apidae bees (Figure 3.22). There were no significant differences in Apidae abundance among sites. That means different sites had the same number of Apidae bees (Figure 3.23).

Table 3.7. Mean number of Apidae bees per collection periods among species

		Mean number of bees per collection periods	
Genus	**Species**	**2011**	**2012**
Anthophora	*bomboides*		1
	terminalis	1	
Apis	*mellifera*	2	3.3
Bombus	*bimaculatus*	1	
	borealis	1	
	fervidus		1
	griseocollis	1	2.3
	impatiens	1.3	3.3
	rufocinctus	1	1.3
	sandersoni	1	
	terricola	1	
Ceratina	*calcarata*	3.3	4.4
	dupla	3.2	3.5
	dupla/mikmaqi		9.1
	mikmaqi	5.8	7.9
Melissodes	*desponsa*		2
	druriella		2
Nomada	*bidentate_C*		1
Xylocopa	*virginica*	1	

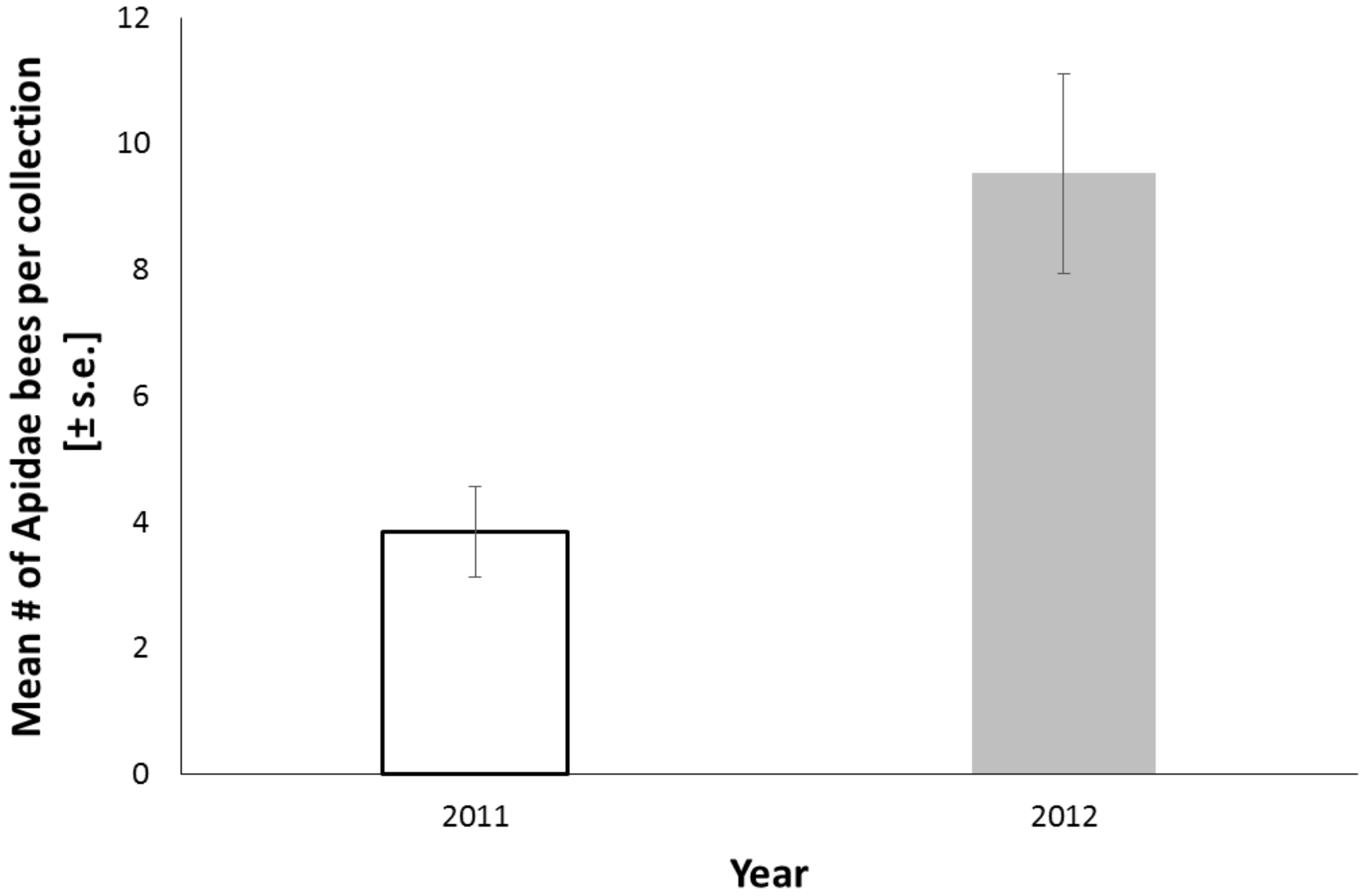


Figure 3.21. The distribution of the mean number of Apidae bees per collection between years. There was no difference in the mean abundance of Apidae between years.

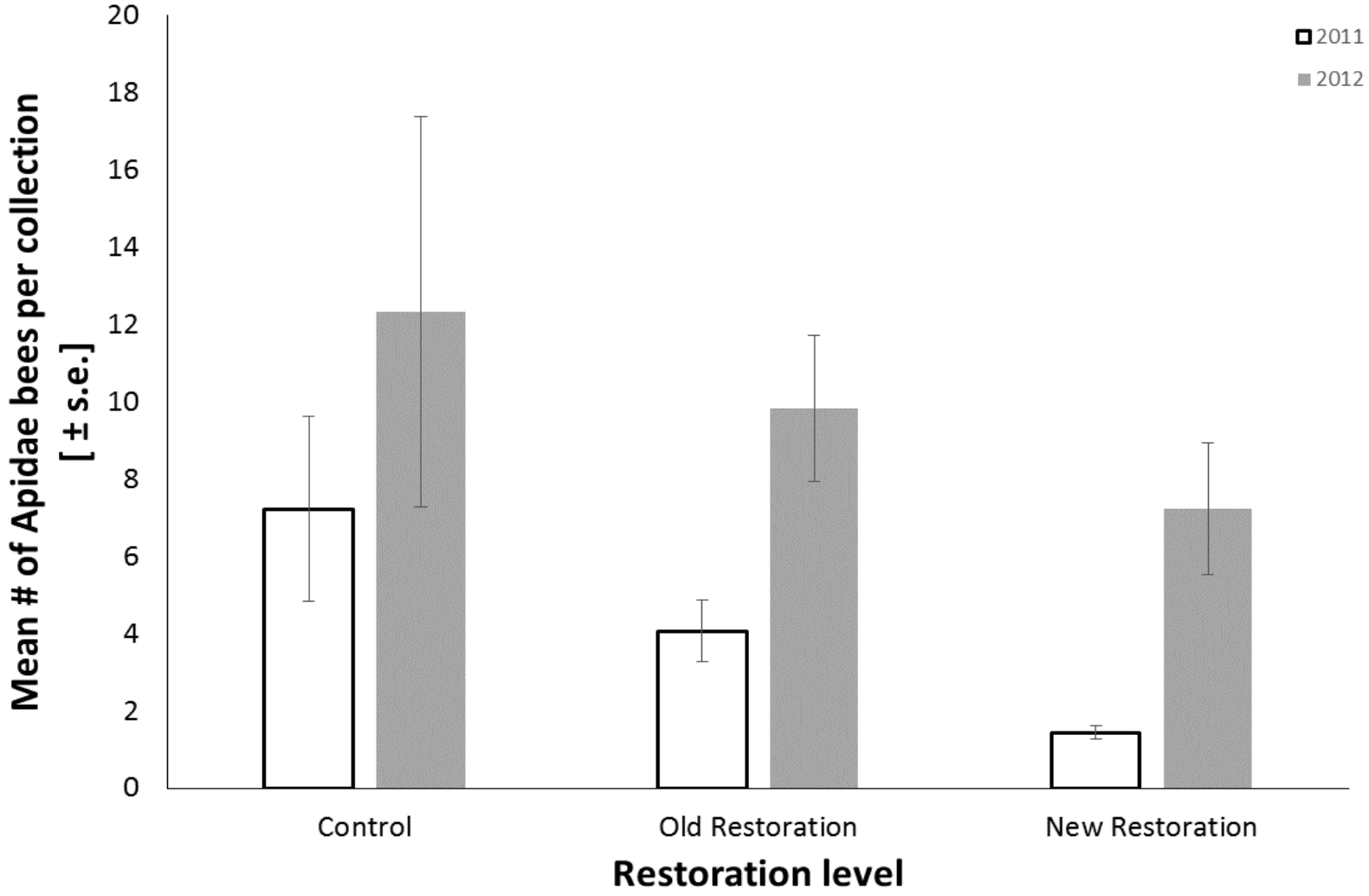


Figure 3.22. The distribution of the mean number of Apidae bees per collection between restoration levels. There was no difference in mean abundance of Apidae among restoration levels. Different restoration levels had the same number of Apidae bees.

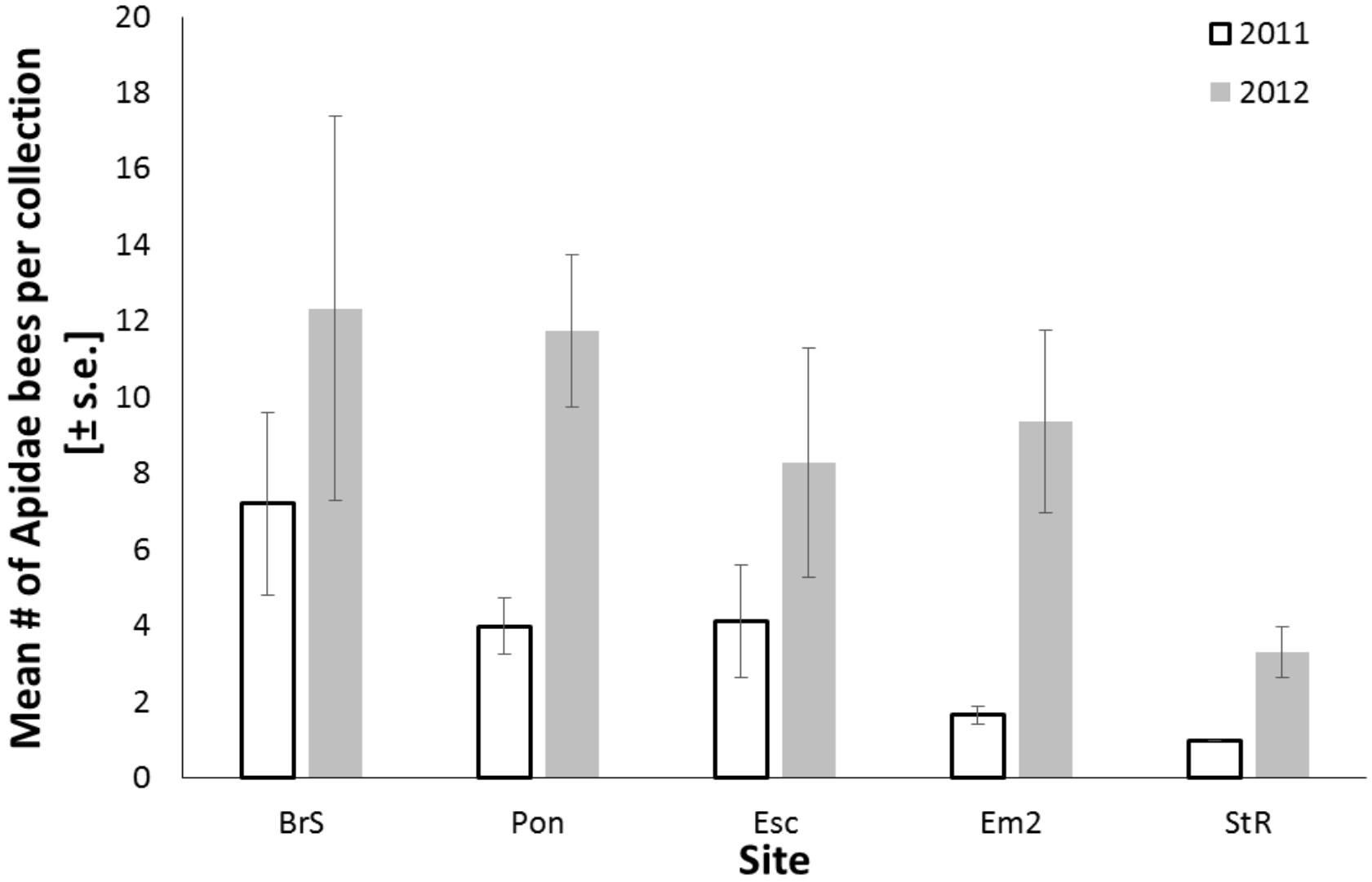


Figure 3.23. The distribution of the mean number of Apidae bees per collection among sites for 2011 and 2012. There was no difference in mean abundance of Apidae among sites.

3.4. Diversity in restored bee communities

For diversity analyses, the 2011 and 2012 surveys were used in all diversity tests at the species level.

3.4.1. Family proportion and patterns in different levels of restoration

The proportions of bee families varied in regard to restoration level. (Fig. 3.24; χ^2= 209.5, *d.f.* = 8, P<0.001). The family Andrenidae represented the least abundant family in all three restoration levels. Apidae and Colletidae were higher in control sites followed by old restoration sites, then the new restoration sites. Apidae and Colletidae abundance increased with restoration time. The family Halictidae represented the most abundant family over the three restoration levels studied. In newly restored sites, 72% of the bees collected were Halictidae. However, Halictidae family decreased to 51% of specimens in old restoration and control sites. Halictidae abundance was higher in new restoration sites than control and old restoration sites. Megachilidae abundance was higher in old restored sites, followed by control sites, then new restoration sites. Halictidae was the most abundant family at all restoration levels.

3.4.2. Species rank abundance

A rank abundance plot of bees collected in 2011 and 2012 by pan traps demonstrates that different species have very different abundances (Figure 3.25; Figure 3.26). The curves showed that few species with high abundance “dominance”, and there were more species with low abundance “rare”.

3.4.3. Variation in species richness among restoration levels

In 2011, the total species richness for all three restoration levels was 62 species. In control site, the total number of species collected was 41 species, while the species richness of old restoration sites was 43 and in the new restoration sites was highest with 47 species. In 2012, the species richness for all three restoration levels was 67 species. The control sites had 34 species, while the old restoration had 36 species and the new restoration sites had 40 species. A huge decline in bee populations was noticed at all sites in 2012.

Randomisation analysis

The observed species richness values were compared to the expected species richness among sites and restoration levels, accounting for differences in sample size by using the randomisation analysis program and the rarefaction curves. The number of species collected in 2011 was not significantly different than expected for BrS, Pon, Em2, control, old restoration level and new restoration sites, while the number of species collected in Esc were significantly lower than expected by abundance (Table 3.8). In Esc the species richness was lower than expected, falling below the predicted range. Esc had more *Augochlorella* (Halictidae) and *Osmia* (Megachilidae) specimens than all other sites, just these two genera represent 56.7% of the total bees (164 bees of 289 bees collected from Esc site). On the other hand, the number of species collected in StR were significantly higher than expected due to the higher number of Halictidae bees underground nester.

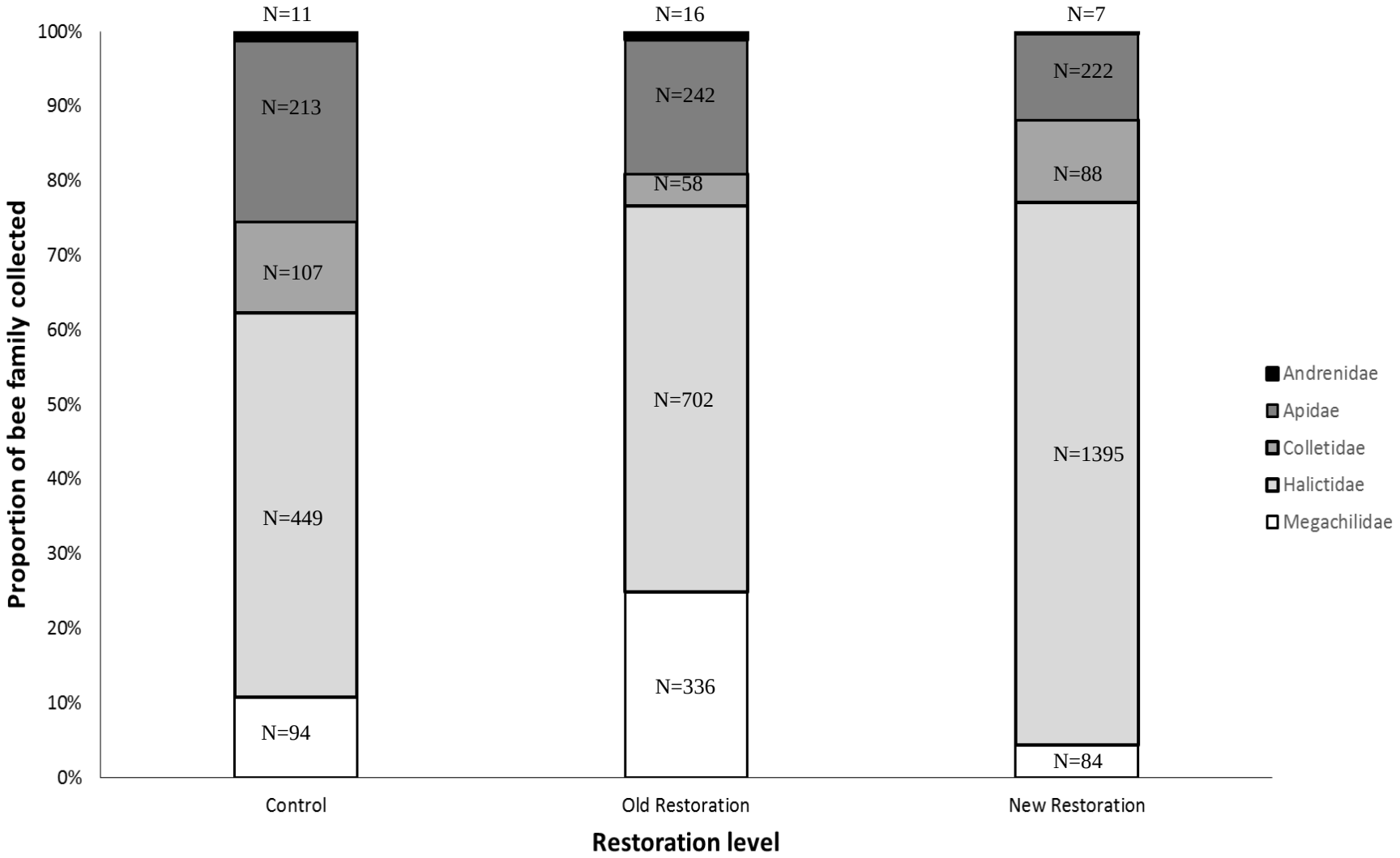


Figure 3.24. Proportions of bee families varied in regard to restoration level.

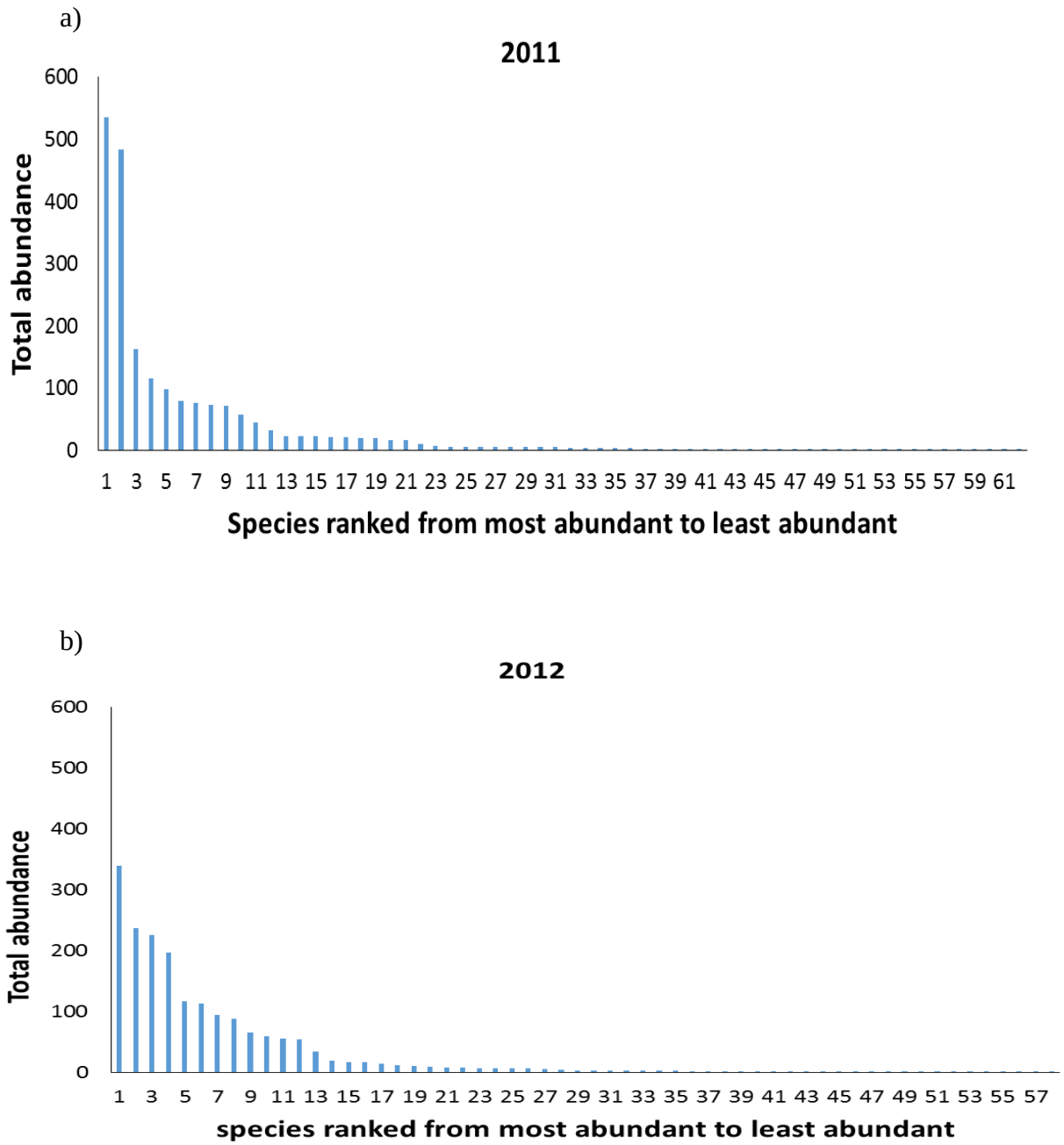


Figure 3.25. a) A rank abundance plot of bees collected in 2011 by pan traps. Twenty-two unidentifiable specimen of subgenus *L. (Dialictus)* were removed. b) A rank abundance plot of bees collected in 2012 by pan traps. Four unidentifiable specimens of subgenus *L. (Dialictus)* and one of *Bombus* were removed.

The number of species collected in 2012 was not significantly different than expected for BrS, Pon, Em2, StR, control site, or new restoration sites, while the number of species collected in Esc and old restoration sites were significantly lower than expected (Table 3.9).

Table 3.8. The mean expected number of species estimated using a randomization analysis of the 2011 complete species list. Twenty-two specimens belonging to the subgenus *L. (Dialictus)* were removed from the species list of 2011 because they were badly damaged and unidentifiable to species level. The observed species richness was compared to the 95% C.I. of the expected frequency distribution. When the observed species richness values fell within the 95% C.I., there were not significant differences between the observed and mean expected values. Alternatively, significant differences between the observed and the mean expected species richness existed when the observed values (**in bold**) fell outside the 95% C.I.

Site/Restoration level	Abundance	Observed # of species	Mean expected # of species	Standard deviation	Lower 95% C.I.	Upper 95% C.I.
BrS/ Control Site	406	41	37.8	2.7	32.4	43.1
Esc	289	**28**	35.8	2.7	30.4	41.2
Pon	403	34	30.8	2.7	25.5	36.1
Em2	515	35	39.7	2.7	34.4	45.0
StR	506	**35**	28.8	2.7	23.6	34.0
Old Restoration Sites	692	43	42.6	2.6	37.5	47.8
New Restoration Sites	1022	47	44.6	2.6	39.5	49.7

Table 3.9. The mean expected number of species estimated using a randomization analysis of the 2012 complete species list. Four specimens belonging to subgenus *L. (Dialictus)* and one specimen belong to *Bombus* were removed from the species list of 2012 because they were badly damaged and unidentifiable to species level. The observed species richness was compared to the 95% C.I. of the expected frequency distribution. When the observed species richness values fell within the 95% C.I., there were not significant differences between the observed and mean expected values. Alternatively, significant differences between the observed and the mean expected species richness existed when the observed values (**in bold**) fell outside the 95% C.I.

Site/Restoration level	Abundance	Observed # of species	Mean expected # of species	Standard deviation	Lower 95% C.I.	Upper 95% C.I.
BrS/ Control Site	463	34	37.7	2.7	32.4	43.1
Esc	396	**24**	35.8	2.7	30.4	41.2
Pon	262	29	30.8	2.7	25.5	36.1
Em2	535	35	39.7	2.7	34.4	45.0
StR	220	27	28.8	2.7	23.6	34.0
Old Restoration Sites	658	**36**	42.6	2.6	37.5	47.8
New Restoration Sites	755	40	44.5	2.6	39.5	49.7

Rarefaction analysis

These restoration variation patterns identified in the previous section were also identified in the rarefaction curves of 2011 and 2012 species that were calculated for the three restoration levels and for each restoration level biweekly.

In 2011, the overall species richness of the three restoration levels had 62 species. The control level, with 408 bees and about 42 species, yielded the highest species richness per number of individuals collected when the three restoration levels studied were compared at the cut-off of 408 bees. The control level with 408 bees and about 42 species yielded the highest species richness per number of individuals collected, contributing the most to the species richness of the three restoration levels studied. The slope of the curve for restored control at the cut-off of 408 bees was 37 species. The lowest species richness was the restored site with 34 species (Figure 3.26).

In 2012, the overall species richness of the three restoration levels was 59 species. The new restoration sites yielded the most abundance with 757 specimens and the highest species richness with 41 species, followed by the old restoration sites which had 37 species with 660 individuals, and then the control site which had 35 species with 464 individuals. When the cut-off point of the lowest sample size of the control site (464) was used, the new restoration sites had 36 species, followed by the control site which had 35 species, followed by the old restoration level which had 33 species (Figure 3.27).

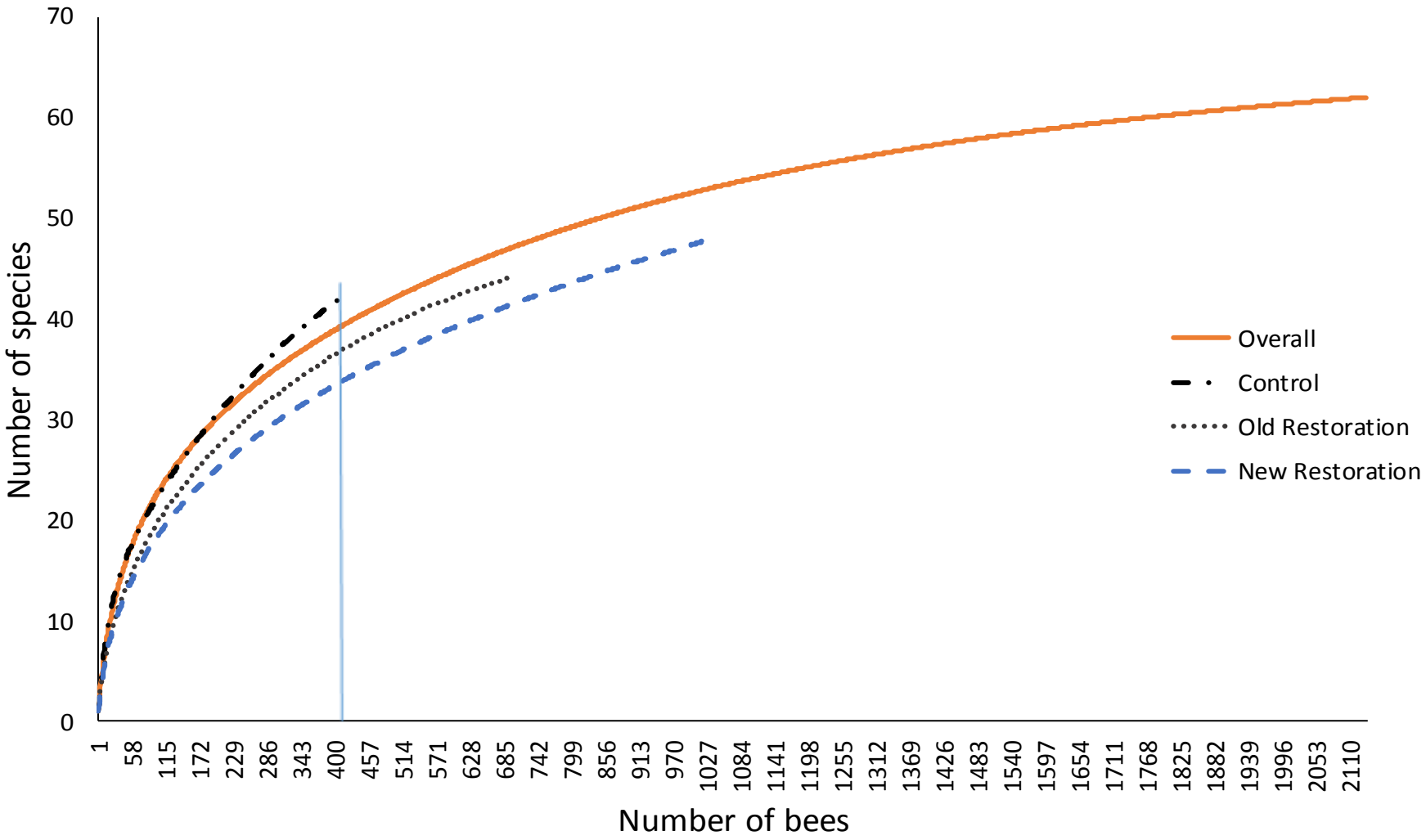


Figure 3.26. Rarefaction curves for the three restoration level comparing the number of species collected biweekly at six sites in 2011. The vertical line represents the sample size of the control level (408 bees) which was used to compare species richness variation among restoration levels.

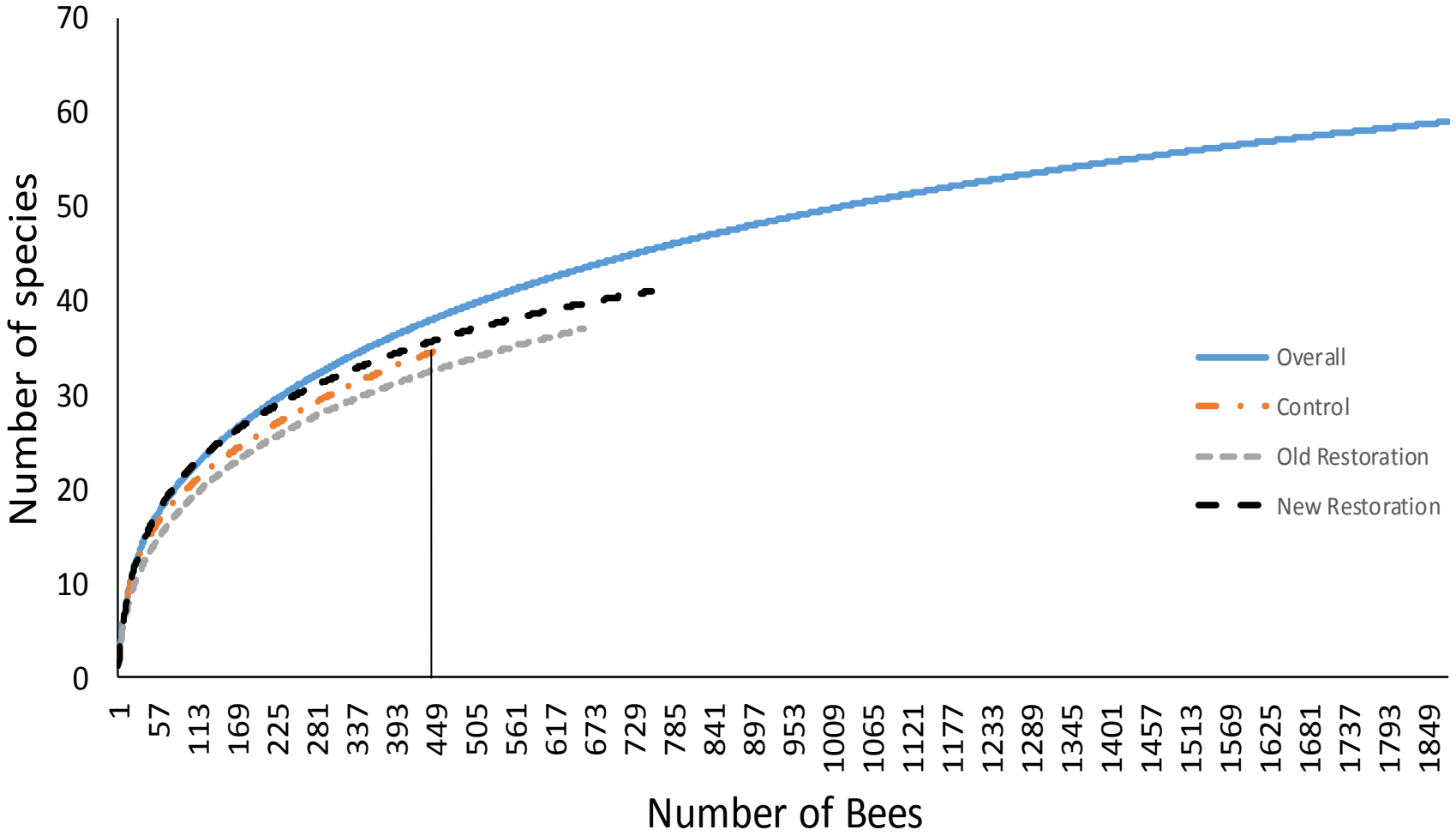


Figure 3.27. Rarefaction curves for the three restoration level comparing the number of species collected biweekly at six sites in 2012. The vertical line represents the sample size of the control level (464 bees) which was used to compare species richness variation among restoration levels.

3.5. Flower collections

3.5.1. Flower collections of 2011

Bees were collected from 18 different types of wildflowers. The availability of each flower species was estimated as the total number of sites where the flowers were sampled for bees. The diversity of flowers growing in patches large enough for 5 minute sampling was highest in the old restoration level (N = 15 flower species), followed by control (N = 12 flower species), followed by new restoration (N = 11 flower species) (Table 3.10.). There was one flower species (*Polygonum sp*.) exclusive to the control level, four flower species (*Euphorbia esula, Linum lewisii, Melilotus officinalis* and *Rosa sp*.) exclusive to the old restoration level, and one flower species exclusive to the new restoration level (*Lotus corniculatus*). *Aster novae-angliae, Cichorium intybus, Daucus carota, Dipsacus fullonum, Linaria vulgare, Erigeron philadelphicus, Solidago* flat and *Trifolium pratense* were found in all restoration levels.

At the control site, 40 flower collections were made, 42 flower collections were made at the old restoration sites, and 54 flower collections were made at the new restoration sites. The number of collections was highest in the new restoration levels, but this level had three sites while the control level and old restoration level had single sites.

When the number of bees per sample was compared between the three restoration levels, it was clear the old restoration level and new restoration level had the highest number of bees. This suggests there were more blooming flowers available for bees to forage on at this sites (Figure 3.28).

Fifty-five bee species were collected in flower samples. The minimum number of flower species that each bee species collected from was four for the following species:

Table 3.10. Flower species, number of samples for each flower species and the abundance of bees per sample in the BrS, GQNS, Em1, Em2, and StR sites of 2011.

	Restoration level and field site											
	Control		Old Restoration		New Restoration							
	BrS		GQNS		Em1		Em2		StR			
Flower species	Bee abundance	No. of samples	Bee abundance	No. of samples	Bee abundance	No. of samples	Bee abundance	No. of samples	Bee abundance	No. of samples	Total bee abundance	Total samples
Aster novae-angliae	2	1	11	2			7	2			20	5
Convolvulus arvense	116	18	92	8							208	26
Cichorium intybus	8	2	4	1	1	1	3	1	4	1	20	6
Coronilla varia	11	2	28	5							39	7
Daucus carota	52	10	49	7	4	1	14	3	20	1	139	22
Dipsacus fullonum	26	5	4	1			17	4			47	10
Euphorbia esula			22	3							22	3
Erigeron philadlphicus	31	2	15	2			26	3	1	1	73	8
Linaria vulgare	3	1	44	4			5	3			52	8
Lotus corniculatus					1	1	12	7			13	8
Linum lewisii			3	1							3	1
Melilotus alba			61	7	6	1	38	5	6	1	111	14
Melilotus officinalis			8	1							8	1
Polygonum pensylvanicum	28	1									28	1
Rosa sp.			1	1							1	1
Solidago flat	28	2	21	3			77	9			126	14
Trifolium pratense	17	4	2	1			12	3	98	8	129	16
Vicia cracca	8	4					15	3			23	7
Grand Total	330	52	365	47	12	4	226	43	129	12	1062	158
Number of bees per sample	6.35		7.76		6.22							

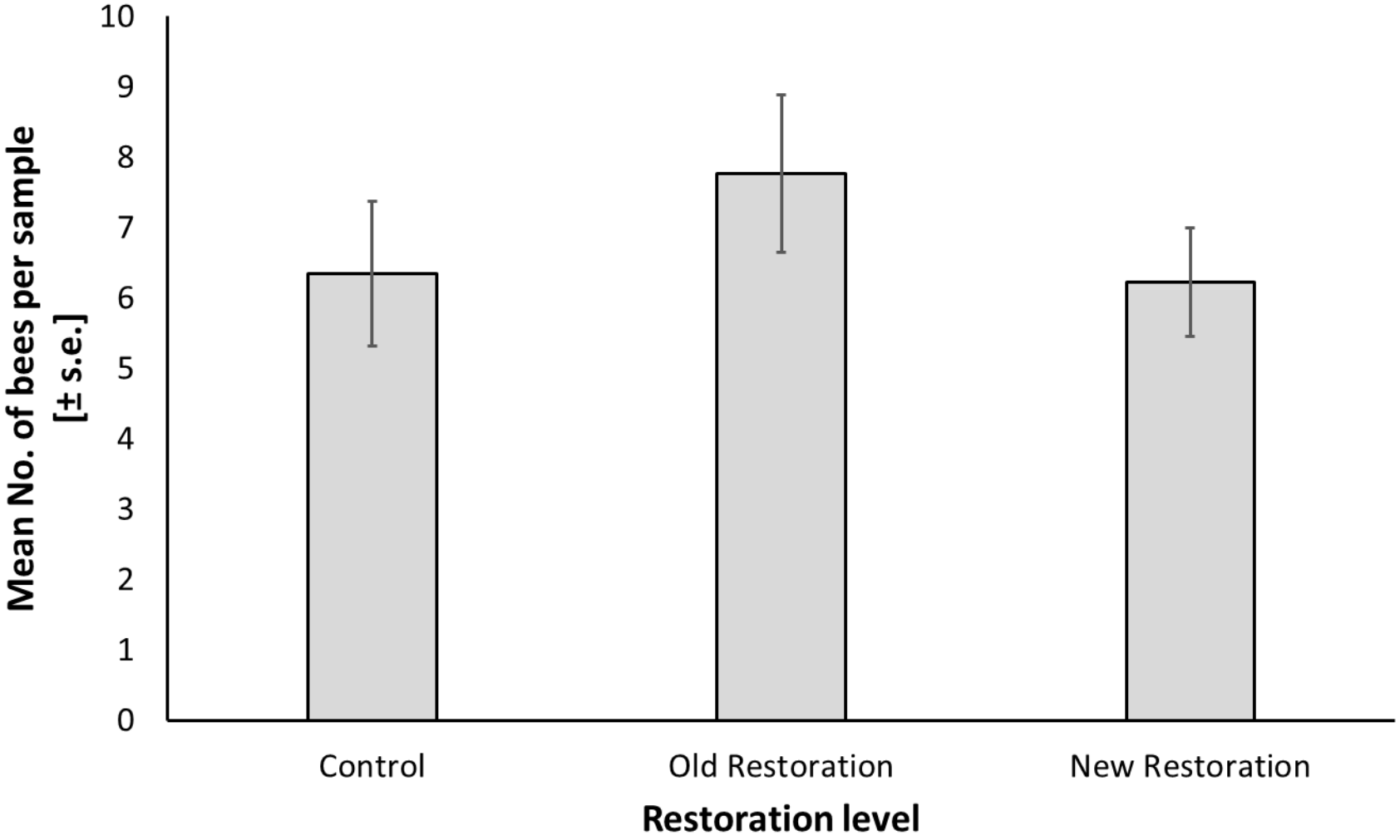


Figure 3.28. Mean number of bees per sample among restoration levels of 2011. There was a difference in mean number of bees per sample among restoration level of 2011. The old restoration and the new restoration levels had the highest bee abundance, followed by the control level.

Apis mellifera, Bombus impatiens, Halictus ligatus, Augochlora pura, L. (Dialictus) versatum, Hylaeus modestum, Augochlorella aurata, Hylause affinis, and *Bombus bimaculatus* (Figure 3.29). The flower species bees most preferred was *Polygonum sp.* which yielded 208 individual bees (Figure 3.30).

3.5.2. Flower collections of 2012

Bees were collected from 20 different types of wildflowers. The availability of each flower species was estimated as the total number of sites where the flower was sampled for bees. The new restored level of restoration had the most flower species (N = 15), followed by restored control (N = 12), followed by control (N = 11) (Table 3.11.). There was one flower species (*Rosa sp*.) exclusive to the control level, two flower species (*Aster novae-angliae,* and *polygonum)* were exclusive to the old restoration level, and six flower species were exclusive to the new restored level (*A. fruticosa, C. intybus, Hieracium sp., L. lewisii, M. officinalis,* and *T. pratense). C. arvense, C. varia, D. fullonum, Erigeron sp., L. corniculatus* and *M. alba* were the only flower species that were found in all restoration levels.

I made 49 flower collections at the control level, 36 flower collections at the restored control level, and 54 flower collections at the restored level. The number of collections was highest in the new restoration level which had three sites: Em1, Em2, and StR, while the control level, and old restoration level had single sites.

When the number of bees per sample was compared between the three restoration levels, it became clear that the old restoration level had the highest number of bees, which suggests there were more blooming flowers available for bees to forage on at this level (Figure 3.31).

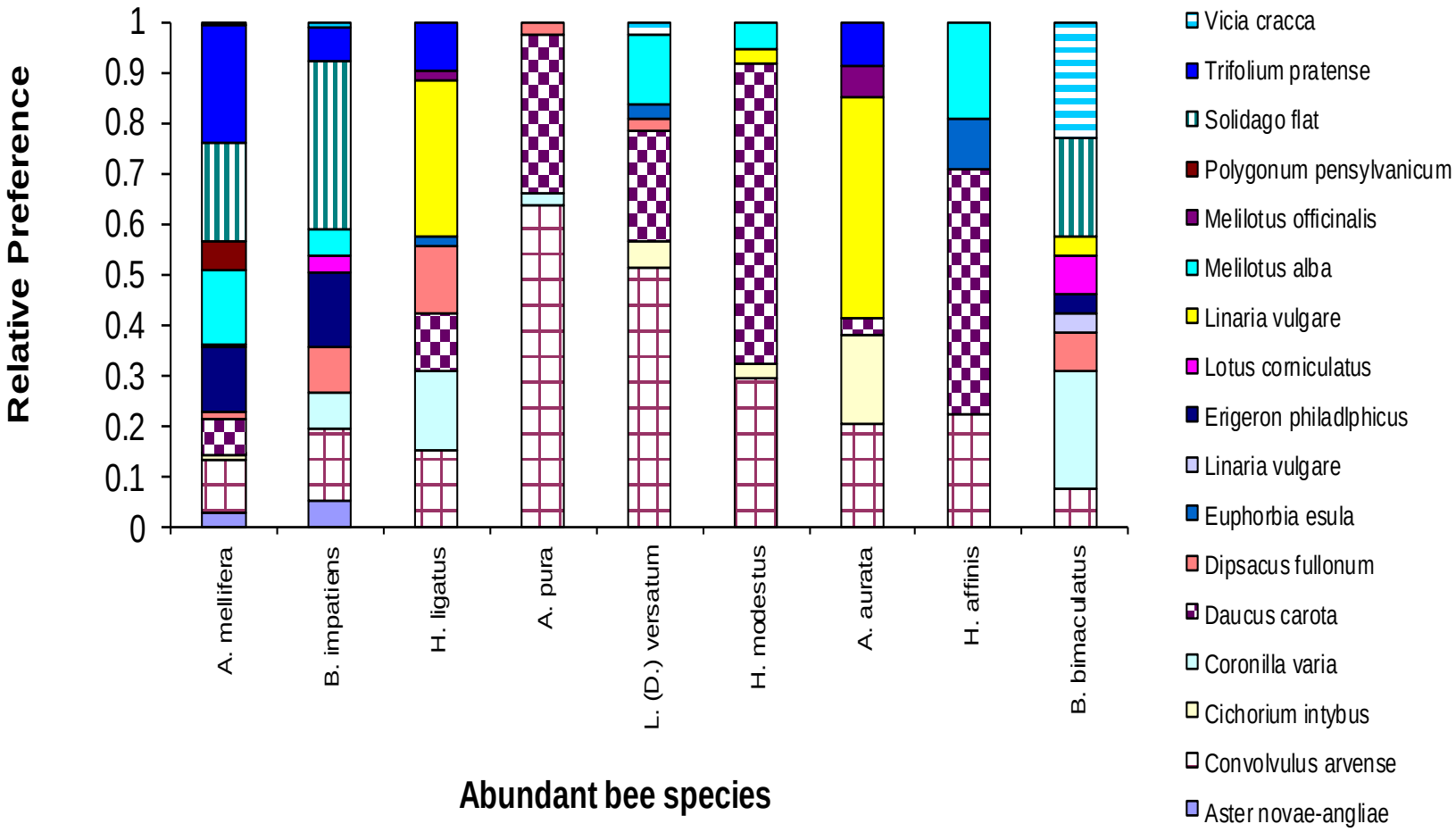


Figure 3.29. Relative wildflower preferences for abundant bee species of 2011.The nine bee species were the most abundant species among all collected bees, which comprised 74.8% of total bees collected in 2011.

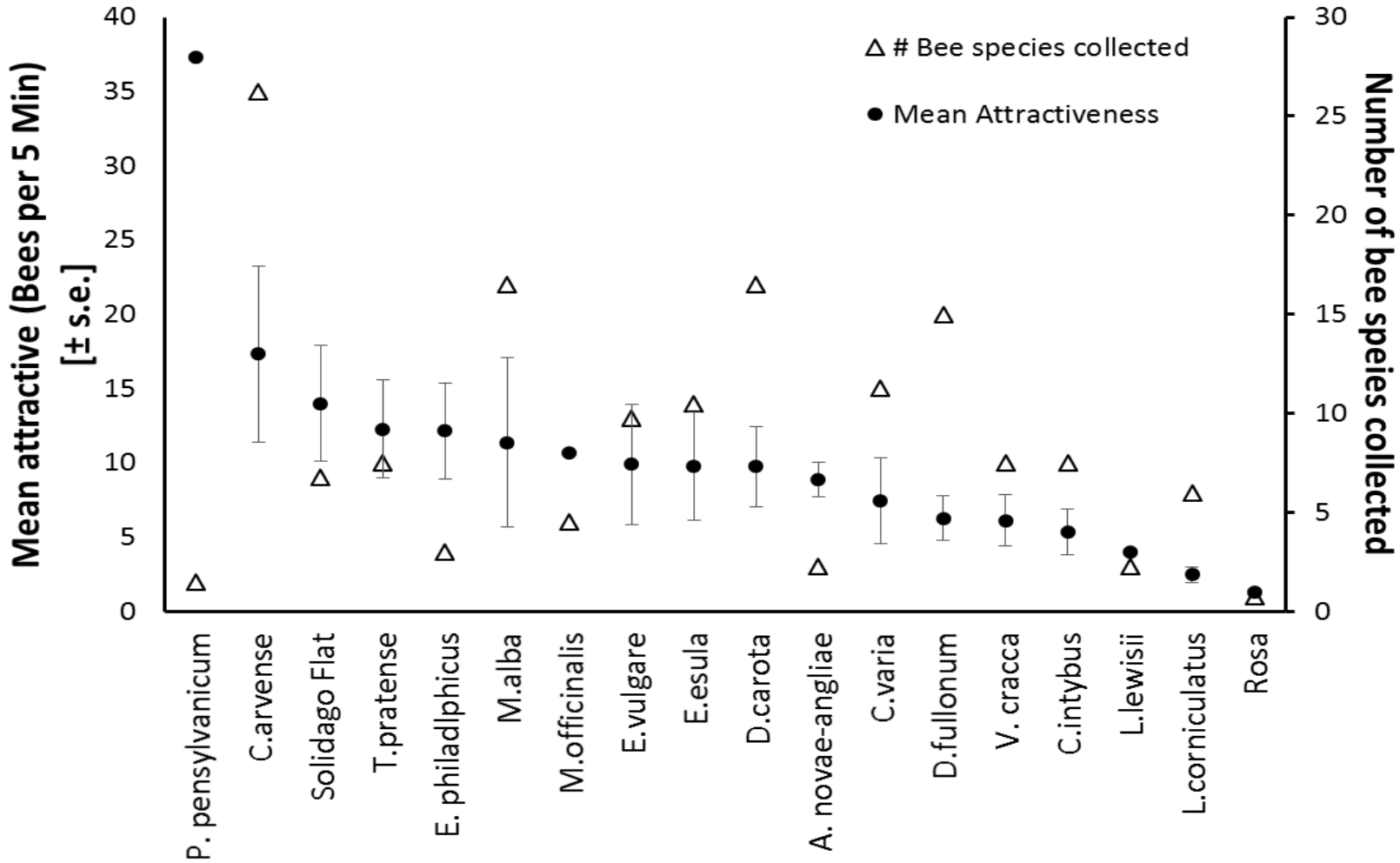


Figure 3.30. The mean attractiveness of wildflowers to bees of 2011 (± s.e.) and the number of bee species collected on each the wildflower species. Mean attractiveness was the average number of bees collected from that wildflower species per five minute collection period.

Table 3.11. Flower species, number of samples for each flower species and the abundance of bees per sample in the BrS, GQNS, Em1, Em2, and StR sites of 2012.

	Restoration level and field site											
	Control		Old Restoration		New Restoration							
	BrS		GQNS		Em1		Em2		StR		Total bee abundance	Total samples
Flower species	Bee abundance	No. of samples	Bee abundance	No. of samples	Bee abundance	No. of samples	Bee abundance	No. of samples	Bee abundance	No. of samples		
Amorpha fruticosa							11	1			11	1
Aster novae-angliae			20	1							20	1
Centaurea nigra	128	10	215	10							343	20
Convolvulus arvense	3	2	5	3	2	1					10	6
Cichorium intybus							4	1			4	1
Coronilla varia			14	2	2	1			3	1	19	4
Daucus carota	10	3							12	3	22	6
Dipsacus fullonum	174	16	20	2					24	3	218	21
Erigeron philadlphicus	40	10	11	1	12	2					63	13
Hieracium canadense									5	1	5	1
Linaria vulgare	37	7	19	4	2	1	3	1			61	13
Linum lewisii					2	1					2	1
Lotus corniculatus	3	1	3	2			18	2			24	5
Melilotus alba	17	2	73	5	137	14	68	8	66	6	361	35
Melilotus officinalis									22	4	22	4
Polygonum pensylvanicum			7	4							7	4
Rosa sp.	6	1									6	1
Thlaspi arvense					8	1					8	1
Trifolium pratense			9	2			7	1	44	9	60	12
Vicia cracca	3	2	7	1							10	3
Grand Total	421	54	403	37	165	21	111	14	176	27	1276	153
Number of bees per sample	7.80		10.89		7.29							

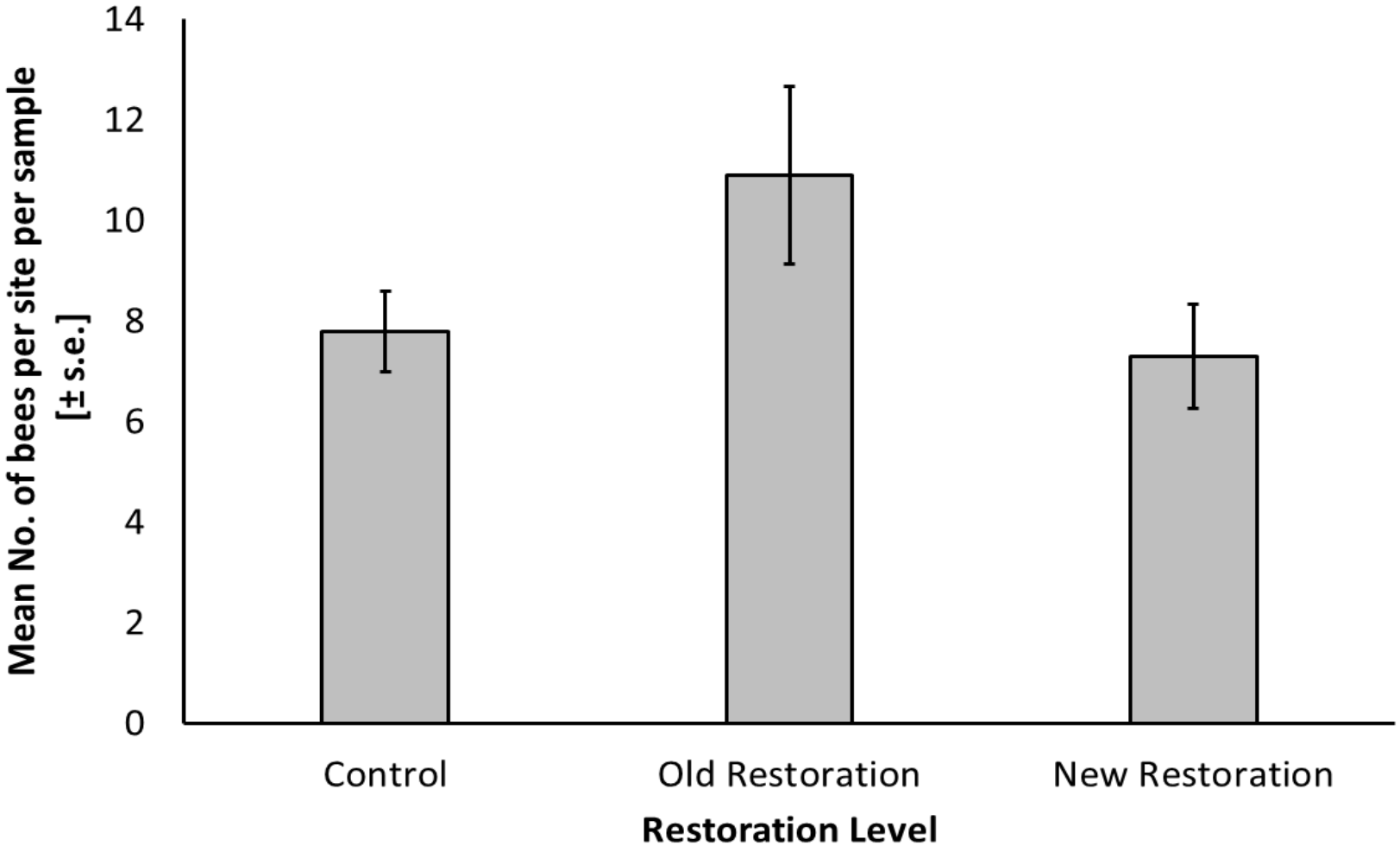


Figure 3.31. Mean number of bees per SAMPLE between restoration levels in 2012. There was a difference in mean number of bees per sample among restoration levels in 2012. The old restoration had the highest bee abundance, followed by the control, then the new restoration sites.

Fifty-two bee species were collected in 2012 flower samples. The most abundant species were: *Apis mellifera, Bombus griseocllis, Bombus impatiens, Ceratina dupla/mikmaqi, Augochlorella aurata, Melissodes desponsa, Andrena sp.,Bombus rufocinctys, Halictus ligatus,* and *Hylause affinisn.* These species were the most abundant species within the 2012 flower collection and comprised 85% of all bees collected (Figure 3.32). The flower species bees preferred most was *C. nigra,* which yielded 208 individual bees, while the flower species which had the highest diversity of bee visitors was *M. alba (*Figure 3.33). The flower species bees preferred the most was *M. alba,* which yielded 361 individuals of bees (Figure 3.33).

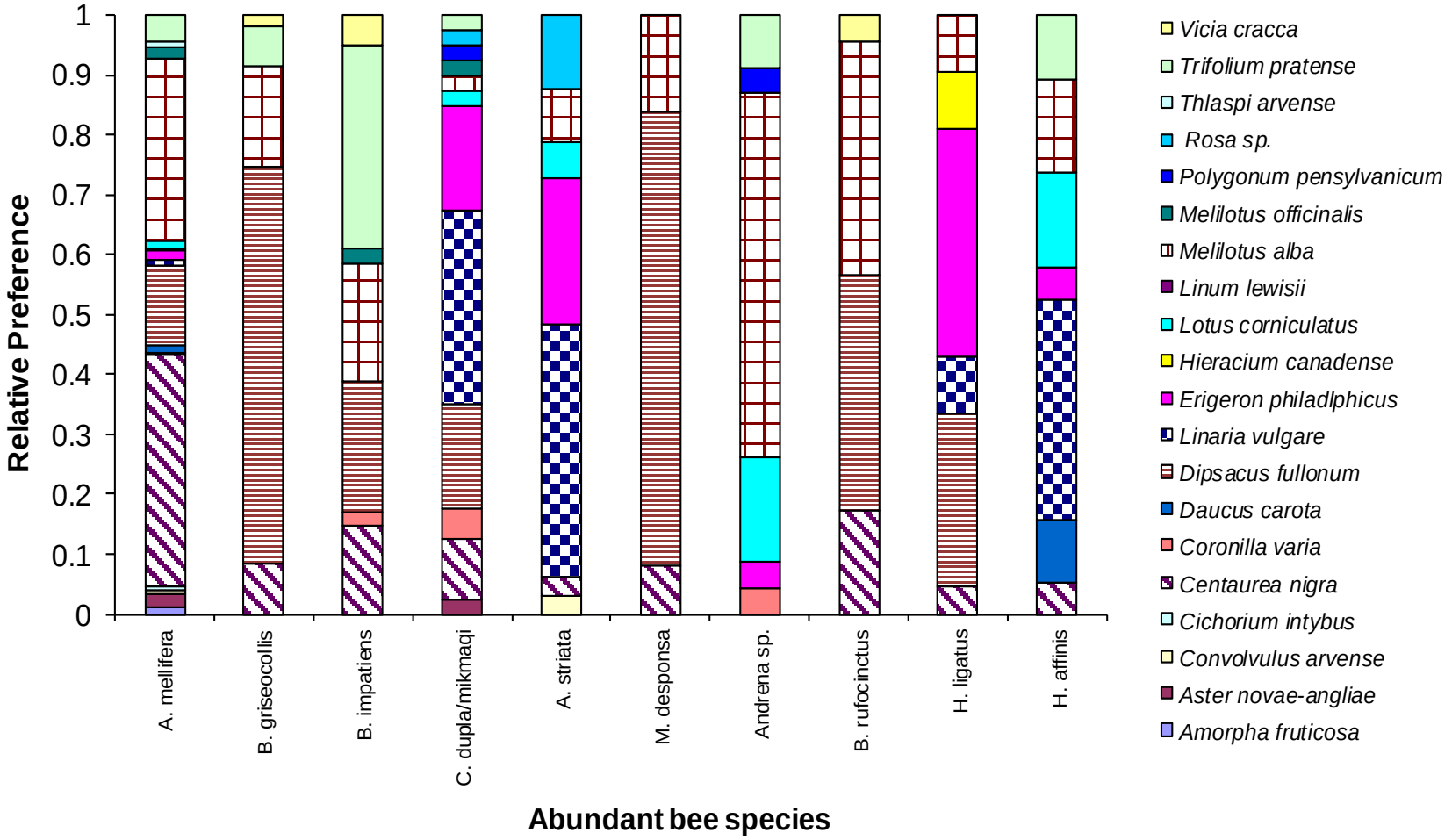


Figure 3.32. Relative wildflower preferences for abundant bee species of 2012. The ten bee species presented in this figure were the most abundant species among all collected bees, comprising 85% of total bees collected in 2012.

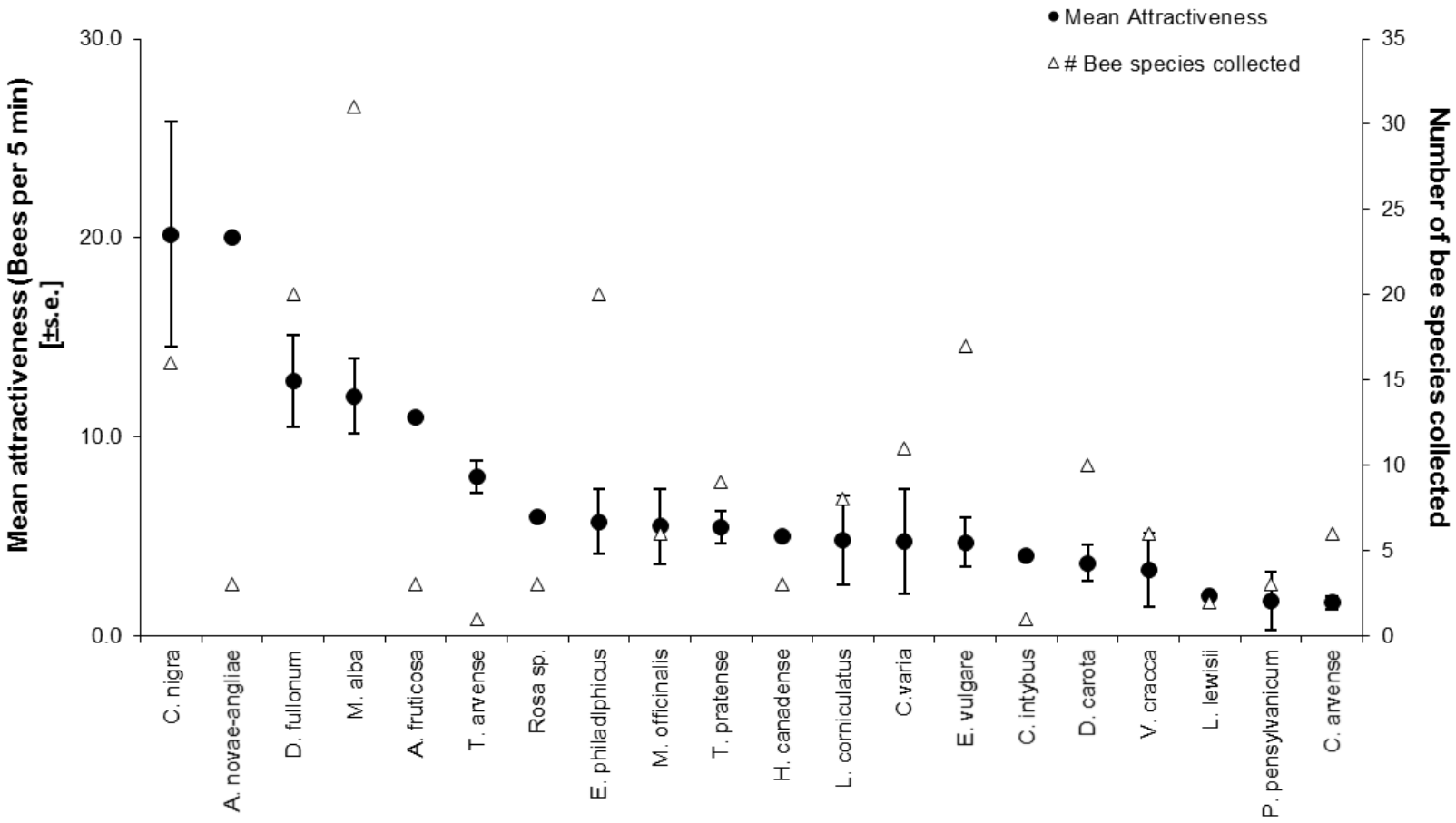


Figure 3.33. The mean attractiveness of wildflowers to bees of 2012 (± s.e.) and the number of bee species collected on each wildflower species. Mean attractiveness is the average number of bees collected from that wildflower species per five minute collection period.

4. Discussion

Over the three restoration levels, bee abundance and diversity were not as low as expected in the restored land filled sites sampled in southern Ontario. Species abundance showed high variability within and between restoration levels. My results suggest that landfill restoration led to major increases in bee abundance and species diversity in both the Elm Street and Station Road Naturalization Sites.

4.1. General aspects of bee community

I collected 4,023 bee specimens, which represented the majority of bee species from the Niagara region restored landfills species. The bee community in the restored landfill sites of Niagara was very diverse and contained five families (Apidae, Andrenidae, Colletidae, Halictidae, and Megachilidae) found in North America, 25 genera and sub-genera, and at least 80 species.

In Niagara, many species are rare and few are abundant. This result matches with bee assemblages in St. Catharines (Richards et al 2011). The following represent species that are new records in Niagara region when the species lists of 2011 and 2012 are compared with the species lists of the Niagara region from 2003 to 2010: *Agapostemon texanus, Andrena fragilis, Andrena integra, Andrena vicina, Bombus borealis, Bombus sandersoni, Bombus terricola, L. (Dialictus) pilosum,* and *Megachile sculpturalis.*

4.2. Community temporal variation

Two distinct bee seasons were found in Niagara in 2011 and 2012: spring and summer. Some bee families are better studied late or early in the season depending on the flower availability, bee pollen, and nectar requirements. For instance, most Andrenidae were found in the early spring. The spring was divided into early spring and late spring.

The early spring was dominated by bees that overwinter as adults such as *Osmia conjuncta,* while the late spring was dominated by *Augochlorella aurata,* a eusocial ground nester. This result matches with Richards et al. (2011) phenology study. Summer bees are usually newly emerged adults which overwinter as larvae or pupae, notably Andrenids. León Cordero (2011) described week 11 as "flight activity quiescent periods" for bivoltine and eusocial bees because this period was following a period of provisioning and preceding emergence or the worker brood. Weather has a major influence in bee behaviour and life cycle (Ginsberg, 1983).

Generally, the flight activity in control and new restoration sites was higher than in old restoration sites. The patterns of bee flight activity were varied and changed during the collection period. Also, bees were more abundant in spring than summer.

4.3. Abundance and diversity of the bee community

Based on the carrying capacity hypothesis and the intermediate disturbance hypothesis, I had predicted two patterns of bee abundance. The first pattern predicted that bee abundance would increase dramatically and then become stable as bee populations reach carrying capacity. Based on the intermediate disturbance hypothesis, I expected to see the highest abundance at the old restoration sites, followed by the control site, and then the new restoration sites. The intermediate disturbance hypothesis was not supported in this study. Based on the increased disturbance hypothesis, I had predicted a second pattern where bee abundance and diversity would increase as disturbance decreased. Based on this hypothesis, the new restoration sites would show low numbers of bees. I found that bee abundance was evenly distributed among restoration levels. Different restoration levels showed the same levels of bee abundance which proves that restoration

is positively increasing the abundance of bees in the new restoration sites. This study shows no difference in bee abundance between control and new restored sites.

The bee diversity pattern with respect to restoration level was not as I had predicted. Based on the intermediate disturbance hypothesis, I had predicted that the highest species richness should be present at the old restoration sites, and lower species richness should be present at the control, and finally even lower at the new restoration sites. The second predicted pattern following the increased disturbance hypothesis was that the highest diversity should occur in the control sites. However, the species richness pattern was different than expected. The highest species richness was found at the new restoration sites followed by the control site, and then the old restoration sites. The different pattern was a result of the different number of bees collected in different levels. To solve this problem in sample size, a randomization analysis was used. In 2011, the randomization analysis indicated that there were significant differences between observed and expected species richness for Esc and StR sites. Esc observed species richness was lower than the expected species richness due to the low number of bees caught from this site in 2011 with only 289 specimens while StR sites was higher in observed species richness than the expected due to the high number of bees collected from this site with 692 specimens. In 2012, the Esc site and old restoration level in total had lower observed species richness than expected species richness and that also was based on abundance, so the composition of these assemblages was significantly different. The different patterns of bee abundance and diversity indicate the species richness at each site and restoration level were simply a result of the number of bees caught.

The effects of biweekly collection periods, family, restoration level, and site on overall abundance and abundance of each family were separately studied. Date, in this study each biweekly collection period, is known to be a major factor that influences bee abundance and diversity. This is because weather and the seasons changed during the study. The bee community abundance also varied by year, restoration level and site. My results highlight how restoration of landfills sites was the main reason for increase bee abundance and diversity in the newly restoration sites since succession affects the food and nest resources that bees need to inhabit these sites.

Regarding family, in both years Halictidae was the most abundant family, while Andrenidae was the least abundance. In 2011 there were so many halictids specially underground nesters in the new restoration sites were the soil is newly mixed and plenty of bare ground are available and the absent of the complex root system in the old ground. In 2012 there were a big decline in all family but Halictidae was the most affected family. The most decline in 2012 was at the new restoration sites: Em2 and StR. Em2 site had to be replanted by the mid-summer of 2011 caused by the low abundance of the vegetation coverage and StR was so middy and they have to dag new artefact pond to get rid of the extra water in this sites. It was likely the result of an overall decline in the number of underground nesters bee (family Halictidae) that failed to recover by the next year 2012.

On the whole, I found that there were no differences in bee abundance among restoration levels. This means the newly restored sites had the same amount of bees as old restoration and control sites. This highlights the important of restoration to increase bee abundance. This situation, in turn, could have surprising implications for ecology and ecosystem conservation, especially for valuable species such as bees. Since Halictidae

was the most abundant family in all restoration levels and, therefore, strongly influenced the overall pattern, I studied each family independently to see the structure of each bee family abundance pattern.

Blossom availability and food resources were two important factors affecting bee abundance. As expected, the availability of blossoms within my study sites was different according to restoration levels. One of the most important differences between the three restoration levels was flower availability. The correlation between the availability of flowers and bees is well studied (Klein et al. 2005; Steffan-Dewenter and Tscharntke 1999; Holzschuh et al. 2007; Hegland & Boeke 2006; Viana & Kleinert 2005; Potts et al. 2003a; Potts et al. 2003b). In 2011, the old restoration sites had the highest number of bee species (46 species), followed by the control (36 species), then the new restoration sites (29 species). These figures were due to the low number of attractive dense flower species in the new sites in the first year after restoration. In 2012, the control and the old restoration sites had the highest bee species (34 species), followed by the new restoration sites (31 species).

Another important resource influencing variation in abundance and diversity among restoration level was bee nesting substrate. As expected in the initial year after restoration, the ground nester bees were more abundant in the new restoration areas since big areas of newly planted ground were available without high density plant roots making creating burrows harder in later stages of succession. Also, the heavy clay soil at the control site made digging nests much harder for bees, unlike the new restoration areas where soil had been tilled recently (Richards & Kelly-Rutgers, 2013). Bees have been found to be effective colonizers in newly restored quarrying areas (Heneberge et al. 2012;

Rutgers-Kelly &Richards 2013). Social ground nesters were the highest in abundance followed by cavity nesters, solitary ground nesters, honey bees, bumble bees, and then cleptoparasites. These results match the results of Richards et al. (2011), where the most common nesting substrates were for ground and cavity nester bees. Moreover, the highest proportion of ground nesters occurred in the newly restored sites where there was plenty of open ground, another match with Rutgers-Kelly and Richards' (2013) findings. Cavity nester bees were far less common than ground nesters because most of my study sites were newly restored grass land which had less woody shrubs with pre-existing cavities required for cavity nester bees as suggested in Richards et al. (2011).

4.4. Family proportion and patterns in different levels of restoration

The proportions of bees collected according to family varied in regard to restoration level. I found more bees of Colletidae, Apidae, and Andrenidae in the control site, while new restoration sites had fewer bees of all families except Halictidae. Interestingly, the old restoration sites had more Megachilidae than any other restoration level. In the new restoration level, there were more Halictidae and fewer bees of all other families. This suggests that Megachilidae bees generally avoid areas of high disturbance. Interestingly, areas of intermediate disturbance (old restoration sites) had more Megachilidae bees, but the abundances of other families were lower than expected. This suggests that Megachilidae preferred an intermediate level of disturbance. In my study, a high number of Colletidae were found in the lowest disturbance level (control), while fewer were found in the intermediate and high disturbance levels, suggesting that Colletidae are more sensitive than other bees to restoration level. Corbet (1995) suggested that late succession stages had higher number of Apidae and Megachilidae and

pioneer communities should have more Halictidae; my results support this finding. In the restored control level "intermediate disturbance area", the abundances of Colletidae, Apidae, and Andrenidae families were lower than expected. I expected to see the highest abundance of Megachilidae in the old restoration level based on Potts et al.'s (2003 b) results which show clear evidence of increasing Megachilidae abundance as disturbance level decreased. I found the Megachilidae highest abundance occurred at the old restoration sites. Halictidae were the most abundant family among all restoration levels, suggesting that Halictidae are less sensitive than other bee families. Rutgers-Kelly (2003) suggests pioneer communities should have more Halictidae and late succession stages have more Apidae; these findings also matched my results.

This study confirmed the hypothesis that the number of bees collected according to species would differ among restoration levels. Over the three restoration levels, there was a different pattern in species abundance. This supported the hypothesis that the abundance of most species would change consistently over restoration levels and would move to other abundance categories as the age of sites and level of succession change. Fourteen abundant, common species consistently occurred over the three restoration levels and remained in the same abundance: *A. mellifera, A. pura, B. griseocollis, C. calcarata, H. ligatus, H. confusus, L. (D.) versatum, L. (D.) admirandum, L. (D.) imitatum, L. (D.) ephialtum, L. (D.) viridatum, L. (D.) perpunctatum, M. brevis,* and *O. pumila.*

5. Conclusion

This study focussed on the bee communities found in the initial two years following restoration of landfill sites by recording the reestablishment of bee communities in sites where bees had been eradicated. The results provided solid evidence of the impact of habitat restoration on abundance and diversity of Niagara bee communities in restored landfill sites. Bees showed rapid recolonization in the newly restored sites, since both abundance and diversity of bees reached levels comparable to old restored sites and control sites where bee communities had been long established. The findings of this study regarding bee communities' rapid recovery after disturbance are valuable pieces of knowledge in relation to biodiversity, ecological health, and conservation. Also, knowing how abundance and diversity change in response to disturbance will allow improved management of limited natural resources.

The intermediate disturbance hypothesis and the increased disturbance hypothesis were not supported in this study. Bee abundance in the newly restored sites was higher than expected, so the results showed no significant difference in the bee abundance between restoration levels. Regarding diversity, species richness varied among restoration levels and following the same pattern in 2011 and 2012. The highest species richness was found at the new restoration sites, followed by the old restoration sites, then the control. Yet when the sampling effort was equalized across the restoration levels, the control level had the highest species richness as predicted according to the increased disturbance hypothesis.

Restoration level and succession stage of sites have caused fluctuations in both flowering and the nesting resources for bees which affected bee abundance and diversity

over the two study years (Richards et al. 2011; Richards & Kelly-Rutgers, 2013). The flower collections of 2011 and 2012 showed that the control site had the most abundant bees, followed by the old restoration sites, then the new restored sites. This suggests there were more blooming flowers available for bees to forage on within the control site.

Since the number of bees fluctuated greatly between years across the different restoration levels, future studies should cover the longest possible duration to gain full understanding of variable processes within bee communities. Bee abundance and diversity at the control sites is expected to be stable, while new sites are expected to be changing. At the old restoration sites, abundance and richness is predicted to decline.

Both bee diversity and abundance are highly linked to flower abundance and diversity, as well as bee nesting resources. Flower diversity and abundance and nesting resources were noticeably different across restoration levels, so better measurements of these changes and variation will allow stronger links to the ecological processes affecting bee abundance and diversity.

Also, for future research, I suggest tracking pioneer, late successional species, and body size changes across the restoration levels will add valuable data and insight into Niagara bee communities. Finally, bee samples should be taken from within areas surrounding restoration sites as bees in these areas will migrate into the restoration sites.

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Appendix 2.1. The biweekly collection periods of pan traps and dates for each site in 2011 and 2012. X means those sites were sample.

		Year											
		2011						2012					
Collection periods (Biweekly)	**Date**	**BrS**	**Pon**	**Esc**	**Em1**	**Em2**	**StR**	**BrS**	**Pon**	**Esc**	**Em1**	**Em2**	**StR**
-4	3/22/2012							X					
0	4/17/2012										X	X	X
	4/19/2012							X	X	X			
2	5/4/2012										X	X	X
	5/10/2012							X	X	X			
4	5/17/2012										X	X	X
	5/23/2012							X	X	X			
6	5/25/2011	X	X	X									
	5/28/2011				X	X	X						
	5/30/2012										X	X	X
	6/5/2012							X	X	X			
8	6/8/2011	X	X	X									
	6/10/2011				X	X	X						
	6/14/2012										X	X	X
	6/20/2012							X	X	X			
10	6/27/2011	X	X	X	X	X	X						
	6/25/2012												
	6/28/2012										X	X	X
	7/5/2012							X	X	X			
12	7/10/2011				X	X	X						
	7/11/2011	X	X	X									
	7/11/2012										X	X	X
	7/19/2012							X	X	X			
14	7/21/2011	X	X	X									
	7/22/2011				X	X	X						
	7/25/2012										X	X	X
	8/3/2012							X	X	X			
16	8/2/2011	X	X	X									
	8/4/2011				X	X	X						
	8/13/2012							X	X	X			
	8/16/2012										X	X	X
18	8/17/2011	X	X	X									
	8/19/2011				X	X	X						
	8/21/2012										X	X	X
	8/30/2012							X	X	X			
20	8/29/2011	X	X	X									
	9/2/2011				X	X	X						
	9/3/2012										X	X	X
	9/13/2012							X	X	X			
22	9/16/2011	X	X	X									
	9/18/2011				X	X	X						
	9/20/2012										X	X	X
24	10/7/2011	X	X	X									
	10/8/2011				X	X	X						
		10 sets of collections						13 sets of collections					

Appendix 2.2. The flower availability over all samples within each field site. X means those flowers were found in sufficient number to collect bees for five minutes without repeating the same flower twice.

		Year									
		2011					2012				
Biweekly collection period	Flower Species	BrS	GQNS	Em1	Em2	StR	BrS	GQN	Em1	Em2	StR
6	*Euphorbia esula*		X								
	Erigeron philadelphicus							X			
	Linum lewisii		X								
	Linaria vulgaris		X				X	X			
	Lotus corniculatus						X	X			
	Rosa sp.						X				
	Trifolium pratense							X			
	Vicia cracca						X	X			
8	*Coronilla varia*							X			
	Euphorbia esula		X								
	Erigeron philadelphicus						X		X		
	Lotus corniculatus				X			X			
	Linaria vulgaris		X		X			X	X		
	Linum lewisii								X		
	Meliotus officinalis		X								
	Polygonum pensylvanicum							X			
	Rosa sp.		X								
	Trifolium pratense				X						X
	Vicia cracca				X						
10	*Amorpha fruticosa*									X	
	Cichorium intybus									X	
	Convolvulus arvense	X					X	X	X		
	Coronilla varia							X	X		X
	Daucus carota						X				
	Erigeron philadelphicus						X		X		
	Flowers sp.							X			
	Lotus corniculatus				X					X	
	Linaria vulgare						X			X	
	Melilotus alba							X	X		X
	Meliotus officinalis										X
	Trifolium pratense	X								X	X
	Thlaspi arvense								X		
	Vicia cracca	X			X						
12	*Convolvulus arvense*	X	X								
	Cichorium intybus				X						
	Coronilla varia		X								
	Daucus carota										X
	Dipsacus fullonum						X				X
	Erigeron philadelphicus						X				
	Lotus corniculatus			X	X						

Appendix 2.2. Continued

		Year									
		2011					2012				
Biweekly collection period	**Flower Species**	**BrS**	**GQNS**	**Em1**	**Em2**	**StR**	**BrS**	**GQN**	**Em1**	**Em2**	**StR**
12	*Linaria vulgare*	X			X						
	Melilotus alba		X				X		X	X	X
	Meliotus officinalis										X
	Trifolium pratense	X	X								X
	Vicia cracca	X			X						
14	*Aster novae-angliae*							X			
	Convolvulus arvense	X									
	Cichorium intybus			X		X	X				
	Coronilla varia	X	X								
	Centaurea nigra						X	X			
	Daucus carota	X	X		X	X					X
	Dipsacus fullonum	X			X		X				X
	Hieracium canadense										X
	Melilotus alba		X	X	X	X		X	X	X	X
16	*Convolvulus arvense*		X								
	Cichorium intybus	X									
	Centaurea nigra						X	X			
	Daucus carota	X	X		X						
	Dipsacus fullonum	X			X		X	X			
	Melilotus alba		X		X						
18	*Aster novae-angliae*				X						
	Convolvulus arvense	X	X								
	Coronilla varia		X								
	Daucus carota	X	X	X							
	Dipsacus fullonum				X						
	Melilotus alba				X						
	Polygonum	X									
20	*Convolvulus arvense*	X	X								
	Cichorium intybus		X								
	Coronilla varia	X									
	Daucus carota		X								
	Dipsacus fullonum	X	X								
	Erigeron philadelphicus				X						
	Melilotus alba		X								
	Solidago flat				X						
22	*Solidago flat*	X	X		X						
	Trifolium pratense					X					
24	*Aster novae-angliae*	X	X		X						
	Convolvulus arvense	X	X								
	Erigeron philadelphicus	X	X		X	X					
	Solidago flat				X						
	Trifolium pratense				X	X					

Appindex 3.1. Complete list of specimens captured and identified from flower collection in 2011 and 2012 from five sites, Brock South (BrS) at Brock University, (GQNS) at Glenridge Quarry Naturalization Site in St. Catharines, Elm1 (Em1) and Elm 2 (Em2) sites at the Elm Street Naturalization Site in Port Colborne, and Station (StR) at Wainfleet, Ontario.

Family	Genus and subgenus	Species and Author	Old restoration		New restoration				
			Control BrS	GQNS	Em1	Em2	StR	Total	Flower species
Andrenidae	*Andrena*	*cressonii Robertson*		1				1	*E. esula*
		fragilis Smith	1					1	*C. arvense*
		Integra Smith		1				1	*E. esula*
		nasonii Robertson		2				2	*E. esula*
		vicina Smith		1				1	*E. esula*
		wilkella Kirby	5	5		3		13	*C. arvense, C. intybus, C. varia, L. vulgare, M. alba, T. pratense,* and *V. cracca*
		sp.		4	7	7	5	23	*C. varia, Erigeron sp., L. corniculatus, M. alba, Polygonum sp.,* and *T. pratense*
Andrenidae Total			6	14	7	10	5	42	
Apidae	*Anthophora*	*terminalis* Cresson	3					3	*D. fullonum, E. vulgare,* and *M. alba*
	Apis	*mellifera* L.	318	393	127	195	1	1244	*Amorpha fruticosa, Aster novae-angliae, C. arvense, C. intybus, C. nigra, C. arvense, C. intybus, C. varia, D. carota, D. fullonum, Erigeron sp., Flowers, Hieracium sp., L. corniculatus, L. vulgare, M. alba, M. officinalis, Polygonum flat, Solidago sp., T. arvense, T. pratense* and *V. caracca*
	Bombus	*bimaculatus* Cresson	5	8		14	3	30	*C. arvense, C.varia, D.fullonum, Erigeron sp. , L. corniculatus, L. vulgare, M. alba, Solidago sp.,T. pratense,* and *V. cracca*

Appendix 3.1. Continued

Family	Genus and subgenus	Species and Author	Control	Old restoration	New restoration				
			BrS	GQNS	Em1	Em2	StR	Total	Flower species
		borealis Kirby	3		1	1	1	6	*C. arvense, D. fullonum, Erigeron sp., M. alba,* and *Solidago sp.*
		citrinus Smith		1				1	*C. nigra*
		fervidus Fabricius		2	1		2	5	*C. nigra, D. fullonum, L. lewisii,* and *M. officinalis*
		griseocollis (DeGeer)	57	7		6	5	75	*C. nigra, C. arvense, C. varia, D. fullonum, D. carota, D. fullonum, L. corniculatus, M. alba, Polygonum sp., Solidago sp., T. pratense,* and *V. cracca*
		impatiens Cresson	26	38	5	44	21	134	*Aster novae-angliae, C. nigra, C. arvense, C. varia, D. fullonum, Erigeron sp., L. corniculatus, M. alba, M. officinalis, Solidago sp., T. pratense,* and *V. cracca*
		mixtus Cresson	1	3			1	5	*C. arvense and M. alba*
		rufocinctus Cresson	19	9	5		1	34	*C. nigra, C. arvense, C. varia, D. fullonum, L. vulgare, M. alba, T. pratense ,* and *V. cracca*
		ternarius Say	3				3		*C. intybus*
		terricola Kirby			1		1		*D. fullonum*

Appendix 3.1. Continued

Family	Genus and subgenus	Species and Author	Control BrS	Old Restoration GQNS	New Restoration Em1	Em2	StR	Total	Flower species
		vagans Smith	3	3		1	1	8	*C. varia, D. fullonum, L. corniculatus, M. alba* and *T. pretense*
		unidentifiable	1			1		2	*C. nigra* and *M. alba*
	Ceratina	*calcarata* Smith	5	16		1	2	24	*Aster novae-angliae, C. arvense, C. nigra, D. fullonum, E. esula, Erigeron sp., L. vulgare, L. corniculatus, L. lewisii* and *V. cracca*
		dupla L.	1	5				6	*C. arvense, D. fullonum, L. vulgare,* and *L. lewisii*
		dupla/mikmaqi	16	20	1	1	2	40	*Aster novae-angliae, C. nigra, C. varia, D. fullonum, Erigeron sp., L. vulgare, L. corniculatus, M. alba, M. officinalis, Polygonum sp., Rosa sp.,* and *T. pratense*
		mikmaqi Rehan & Sheffield	5	12	1	3		21	*C. arvense, D. carota, D. fullonum, L. vulgare, Solidago sp.,* and *T. pratense*
	Melissodes	*Apicata* Lovell & Cockerell		1				1	*E. vulgare*
		desponsa smith	22	6	1	2	1	32	*C. nigra, C. arvense, C. varia, D. fullonum,* and *M. alba*

Family	Genus and Subgenus	Species and Author	Control BrS	Old restoration GQNS	New Restoration Em1	Em2	StR	Total	Flower species
	Xylocopa	*Virginica* (L.)	1	5		6		12	*L. vulgare, M. alba, Rosa sp., Solidago sp., T. pratense* and *V. cracca*
Apidea total			486	532	142	276	251	1687	
Colletidae	*Hylaeus*	*affinis* Smith	20	22	4	4		50	*C. nigra, C. arvense, D. carota, E. esula, Erigeron sp., L. corniculatus, L. vulgare, M. alba,* and *T. pretense*
		affinis/modestus	2	3	1		1	7	*C. nigra, D. carota, D. fullonum,* and *M. alba*
		Annulatus (L.)	4	2		5		11	*C. arvense, D. carota, E. esula,* and *Solidago sp.*
		hyalinatus Smith	1					1	*Erigeron sp.*
		Illinoisensis Robertson		1				1	*C. varia*
		mesillae Cockerell	9	3	1	2	1	16	*C. arvense, D. carota, D. fullonum, E. esula, Erigeron sp.* and *M. alba*
		modestus Say	26	9	3	6		44	*C. arvense, C. intybus, C. varia, D. carota, D. fullonum, L. vulgare,* and *M. alba*
		punctatus Brulle	1					1	*D. carota*
		unidentifiable	1				1	2	*D. carota* and *M. alba*
Colletidae Total			64	40	9	17	3	133	
Halictidae	*Augochlora*	*Pura* Say	31	17	4	1	5	58	*C. arvense, C. varia, D. carota, D. fullonum, Erigeron sp.* and *M. alba*
	Augochlorella	*Aurata* Smith	36	28	2		1	67	*C. arvense, C. nigra, C.intybus, D. carota, L.*

Appendix 3.1. Continued

Family	Genus and subgenus	Species and Author	Old Control BrS	Old Restoration GQNS	New restoration Em1	New restoration Em2	New restoration StR	total	Species flower
									vulgare, Erigeron sp., L. corniculatus, M. alba, M. officinalis, Rosa sp. and *T. pratense*
	Augochloropsis	*metallica* Fabricius		1				1	*Erigeron sp.*
	Halictus	*confuses* Smith	8	8		1	3	20	*C. nigra, C.arvense, D. carota, D.fullonum, Erigeron sp., L. corniculatus, L. lewisii, L. vulgare, M. alba,* and *M. officinalis.*
		ligatus Say	38	23		5	7	73	*C. nigra, C. arvense, C. varia, D. fullonum, D. carota, L. vulgare, E. esula, Erigeron sp., Hieracium sp., M. alba, M. officinalis,* and *T. pratense*
		rubicundus Christ	5	9	1	1		16	*Amorpha fruticosa, C. intybus, D. carota, E. esula, Erigeron sp. and M. alba*
	L. (Dialictus)	*admirandum* Sandhouse	1	8				9	*C. arvense, D. carota, E. esula, L. vulgare, M. alba,* and *M. officinalis*
		atwoodi Gibbs	3				2	5	*C. arvense, D. fullonum, Erigeron sp.,*and *Hieracium sp.*
		cressonii Robertson			1			1	*M. alba*
		ephialtum Gibbs	3	1		1		5	*C.arvense, C.intybus, C.varia,* and *M.alba*

Appendix 3.1. Continued

Family	Genus and subgenus	Species and Author	Control	Old Restoration	New restoration				
			BrS	GQNS	Em1	Em2	StR	Total	Flower species
		imitatum Smith	11	9				20	*C. arvense, D. carota, D. fullonum, E. esula, Erigeron sp., M. alba, T.pratense,* and *V. cracca*
		laevissimum Smith		4	1	3	14	22	*C. arvense, C. varia, D. fullonum* and *M. alba*
		lineatulum Lovell	3	3				6	*C. arvense, C. intybus, D. carota,* and *M. alba*
		mitchelli Gibbs	3	8		6	1	18	*C. arvense, D. carota, D. fullonum,* and *M. alba*
		nigroviride Graenicher	2					2	*C.arvense*
		nymphaearum Robertson		1				1	*C.arvense*
		oblongum Lovell			1			1	*M. alba*
		paradmirandum Knerer & Atwood				1	1	2	*Amorpha fruticosa* and *M. officinalis*
		versatum Robertson	25	7	2	3	7	44	*C. arvense, C. intybus, D. fullonum, D. carota, E. esula, Erigeron sp., M. alba,* and *V. cracca*
		viridatum Lovell	3	1				4	*C.arvense and V. cracca*
		unidentifiable	7	3	3	6		19	*Aster novae-angliae, C. arvense, D. carota, Erigeron sp., M. alba and Solidago sp.*
	Lasioglossum (Lasioglossum)	*coriaceum* Robertson		2				2	*M. alba* and *M. officinalis*
		zonulum Smith			1			1	*M. alba*
Halictidae Total			181	134	17	29	45	406	
Megachilidae	*Anthidium*	*manicatum* (L.)		7				7	*C. varia, L. vulgare* and *M. alba*

Appendix 3.1. Continued

Family	Genus and subgenus	Species and Author	Control BrS	Old restoration GQNS	New restoration Em1	Em2	StR	Total	Flower species
		oblongatum lliger		10				10	*C. varia, L. vulgare, M. alba* and *Polygonum sp.*
	Coelioxys	*octodentata* Say		1				1	*L. vulgare*
		rufitarsis Smith	1	1				2	*L. vulgare* and *M. alba*
	Heriades	*Leavitti* Crawford	3	1				4	*C.arvense, D.carota* and *D. fullonum*
		variolosa Cresson	1					1	*Erigeron sp.*
	Hoplitis	*pilosifrons* Cresson		1				1	*T. pratense*
	Megachile	*brevis* Say	1	3	1	1	1	7	*D. carota, D. fullonum, L. vulgare, L. corniculatus, M. alba and Polygonum sp.*
		centuncularis Linnaeus				1		1	*L. corniculatus*
		ericetorum Lepeletier		4	1	1		6	*C. varia, D. fullonum, L. vulgare* and *L. lewisii*
		latimanus Say	2			2		4	*C. nigra, C. arvense* and *D. fullonum*
		pugnata Say		3				3	*C. arvense* and *D. carota*
		rotundata (F.)		9				9	*C. varia, D. carota, L. corniculatus* and *M. alba*
		sculpturalis Smith	1					1	*L. vulgare*
		texana Cresson		1				1	*C. varia*
	Osmia	*conjuncta* Cresson	5	11				16	*C. arvense, C. varia, D. fullonum, L. vulgare, E. esula, Erigeron sp., L. corniculatus, M. officinalis, Rosa sp.* and *V. cracca*
Megachilidae Total			14	52	2	5	1	74	
Grand Total			751	772	177	337	305	2342	